

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 21:30:32 ; Search time 2546.98 Seconds
(without alignments)
1764.633 Million cell updates/sec

Title: US-09-786-015-3

Perfect score: 333
Sequence: 1 caggatgtgcagctcagcc.....ccaggtcgcagctcctcgtggt 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estcl:*
10: gb_estc2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_low:*
15: em_gss_pin:*
16: em_gss_vrtc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	275.4	82.7	451	10	BE476752	BE476752 160141 BA
2	269	80.8	515	10	BE476398	BE476398 159628 BA
3	265.8	79.8	495	10	BE485669	BE485669 172803 BA
4	256.2	76.9	564	10	BE589073	BE589073 194817 BA
5	251.2	75.4	655	10	BE691510	BE691510 340705 BA
6	249.6	75.0	467	10	BE590205	BE590205 197215 BA
7	248.2	74.5	493	10	BE87574	BE87574 176397 BA
8	243.4	73.1	467	10	BE68899	BE68899 336848 BA
9	243.2	73.0	496	10	BE476758	BE476758 160150 BA
10	240.2	72.1	484	10	BE689524	BE689524 337633 BA
11	240	72.1	518	10	BE483566	BE483566 169766 BA
12	239.4	71.9	542	10	BE751028	BE751028 202731 MA
13	237.6	71.4	557	10	BE722165	BE722165 190280 MA
14	236.8	71.1	503	10	BE485929	BE485929 173232 BA
15	236.8	71.1	514	10	BE483616	BE483616 169632 BA
16	236.4	71.0	396	10	BE488003	BE488003 177194 BA
17	236	70.9	553	10	BE749919	BE749919 201001 MA

18	235.4	70.7	538	10	BE688590	BE688590 336269 BA
19	235.2	70.6	474	10	BE588329	BE588329 194153 BA
20	235.2	70.6	477	10	BE690381	BE690381 338902 BA
21	235.2	70.6	488	10	BE49441	BE49441 476833 MA
22	235.2	70.6	489	10	BE476453	BE476453 159697 BA
23	235.2	70.6	491	10	BE692788	BE692788 342607 BA
24	234.2	70.3	420	10	BE482648	BE482648 168498 BA
25	233.8	70.2	528	10	BE688615	BE688615 336301 BA
26	233.6	70.2	471	10	BE774840	BE774840 284827 MA
27	232	69.2	517	10	BE483056	BE483056 169073 BA
28	230.4	69.2	557	10	BM088825	BM088825 502373 MA
29	230.2	69.1	413	10	BE478852	BE478852 163292 BA
30	229.2	68.8	363	10	BE231054	BE231054 253265 BA
31	228.6	68.6	417	10	BE688700	BE688700 364148 BA
32	227.2	68.2	508	10	BE481939	BE481939 167555 BA
33	227.2	68.2	623	10	BE692841	BE692841 342685 BA
34	225.6	67.7	541	10	BM087227	BM087227 499922 MA
35	224.2	67.3	396	10	BE482524	BE482524 168348 BA
36	222.8	66.9	586	10	BE688462	BE688462 336092 BA
37	222.6	66.8	562	10	BE48653	BE48653 471154 MA
38	220.8	66.3	513	10	BE483284	BE483284 169398 BA
39	219.8	66.0	458	10	BE484396	BE484396 170935 BA
40	219.2	65.8	508	10	BE481887	BE481887 167492 BA
41	219.2	65.8	549	10	BE691624	BE691624 340869 BA
42	218.8	65.7	386	10	BE692356	BE692356 342021 BA
43	217.6	65.3	466	10	BE478405	BE478405 162646 BA
44	217.6	65.3	518	9	AW462441	AW462441 BE230009A
45	216.2	64.9	476	10	BE690901	BE690901 339802 BA

ALIGNMENTS

RESULT 1
BE476752 451 bp mRNA linear EST 28-AUG-2000
160141 BARC 5BOV Bos taurus cdna 5', mRNA sequence.
BE476752
BE476752.1 GI:9596285

KEYWORDS

EST.

SOURCE

cow.

ORGANISM

Bos taurus

REFERENCE

1 (bases 1 to 451)

AUTHORS

Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.

TITLE

Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cdna library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Sonstegard TS

JOURNAL

USDA, ARS, Beltsville Agricultural Research Center

COMMENT

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

COMMENT

Tel: 301 504 8416

COMMENT

Fax: 301 504 8414

COMMENT

Email: tadselpsi@ars.usda.gov

COMMENT

Single pass sequencing. Bases called and alt-trimmed with phred

COMMENT

v0.980904.e. Vector identified by cross-match with the -minscore 18

COMMENT

and -mismatch 12 options.

COMMENT

PCR Primers

COMMENT

FORWARD: AGGAACAGTATGACCAT

COMMENT

BACKWARD: GTTTTCCAGTACACAG

COMMENT

Plate: 28 row: K column: 18

COMMENT

Seq primer: ATTTAGTGTACACTATAG.

COMMENT

Location/Qualifiers

COMMENT

1..451

COMMENT

/organism="Bos taurus"

COMMENT

/db_xref="taxon:9913"

COMMENT

/clone_lib="BARC 5BOV"

COMMENT

/tissue_type="pooled"

COMMENT

/lab_host="DH10B"

COMMENT

/note="Vector: pCMV SPORTE; Site_1: XbaI; Site_2: XhoI;

Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 75 a 160 c 123 g 93 t

ORIGIN

Query Match 82.7%; Score 275.4; DB 10; Length 451;
Best Local Similarity 89.2%; Pred. No. 1.9e-62;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 cagagatgtgtcagtcagccgtccgtctgtctgtgtgtcccttgagcagaggttccatc 60
|||||
Db 79 CAGGCTGTGCTGACTGACGCGCTCTCCGCTCCGGGTCCTGGGCCAGAGGCTCCATC 138
QY 61 acctgtcttgaaagcagcagcaacattggaagtaattgtctatgtggctgttacaacag 120
|||||
Db 139 ACCTGCTCTGGAAGCAGCAGCAGAGTGGAACTGGCAATTATGTGACTGTGTTCCAACAG 198
QY 121 gtcccaagatcagcccccagactcctcatcagtgtctacaacagatcgagctcgaggatc 180
|||||
Db 199 ATCCGAGATCGGCCCCCAACACCTTCATCTATGTGTCGACAGTCAGCCTCGGGGCTC 258
QY 181 cccgaccgattctccggtctccaggtctgtggaaacacagccacctgaccatcagctgctc 240
|||||
Db 259 CCGGACCGATTCTCCGGCTCCAGGCTCGGAAACACAGCCCTGACCATCAGCTCGCTC 318
QY 241 caggctgaagcagagcgcgattatctgtgcatacgatcaaaagttactcagttggtt 300
|||||
Db 319 CAGGCTGAGGACGAGGAGATTTATTTCTGTGCATCTTATCAGAGTGTGACACAGCGTGT 378
QY 301 ttccgacgagcgagcagcgctgacgcttctggt 333
|||||
Db 379 TTCCGACGCGGACACGCTGACCTGCTCGGT 411

RESULT 2

BEA76398 515 bp mRNA linear EST 28-AUG-2000
LOCUS BEA76398 159628 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BEA76398
ACCESSION BEA76398.1 GI:9595931
VERSION EST.
KEYWORDS
SOURCE
ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 515)
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
Wells, K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psl.barc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 27 row: G column: 1
Seg primer: ATTAGGTGACACTATAG.
Location/Qualifiers

FEATURES

source
1. .515
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"

/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPOR6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

BASE COUNT 98 a 178 c 132 g 107 t

ORIGIN

Query Match 80.8%; Score 269; DB 10; Length 515;
Best Local Similarity 88.0%; Pred. No. 9.7e-61;
Matches 293; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 cagagatgtgtcagtcagccgtccgtctgtctgtgtgtcccttgagcagaggttccatc 60
|||||
Db 87 CAGGCTGTGCTGACTGACCGCTCTCCGCTCCGGGTCCTGGGCCAGAGGCTCCATC 146
QY 61 acctgtcttgaaagcagcagcaacattggaagtaattgtctatgtggctgttacaacag 120
|||||
Db 147 ACCTGCTCTGGAAGCAGCAGCAGAGTGGAACTGGCAATTATGTGACTGTGTTCCAACAG 206
QY 121 gtcccaagatcagcccccagactcctcatcagtgtctacaacagatcgagctcgaggatc 180
|||||
Db 207 ATCCGAGATCGGCCCCCAACACCTTCATCTATGTGTCGACAGTCAGCCTCGGGGCTC 266
QY 181 cccgaccgattctccggtctccaggtctgtggaaacacagccacctgaccatcagctgctc 240
|||||
Db 267 CCGGACCGATTCTCCGGCTCCAGATCTGGGAAACACAGCCCTGACCATCAGCTCGCTC 326
QY 241 caggctgaagcagagcgcgattatctgtgcatacgatcaaaagttactcagttggtt 300
|||||
Db 327 CAGGCTGAGGACGAGGCTGATTTATTTCTGTGCATCTTATCAGAGTGTGACACAGCGTGT 386
QY 301 ttccgacgagcgagcagcgctgacgcttctggt 333
|||||
Db 387 TTCCGACAGGAGCACACTGACCTGCTCGGT 419

RESULT 3

BEA85669 495 bp mRNA linear EST 28-AUG-2000
LOCUS BEA85669 172803 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BEA85669
ACCESSION BEA85669.1 GI:9605202
VERSION EST.
KEYWORDS
SOURCE
ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 495)
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
Wells, K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psl.barc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 132 row: F column: 18
Seg primer: ATTAGGTGACACTATAG.
Location/Qualifiers

FEATURES

source
1. .495

```

/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_id="BARC_5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

```

Query Match	79.8%;	Score 265.8;	DB 10;	Length 495;
Best Local Similarity	87.4%;	Pred. No. 6.7e-60;		
Matches 291; Conservative	0;	Mismatches 42;	Indels 0;	Gaps 0;

[illegible]

	RESULT	4
LOCUS	BE589073	
DEFINITION	194817 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.	EST 28-AUG-2000
ACCESSION	BE589073	
VERSION	BE589073..1	GI:9842112
KEYWORDS	EST.	
SOURCE	COW.	
ORGANISM	Bos taurus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. 1 (bases 1 to 564) Sonstegard,T.S., Capucio,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D. Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library Unpublished (2000) Contact: Sonstegard TS USA, ARS, Beltsville Agricultural Research Center Bldg. 200 Rm 2A, Beltsville, MD 20705, USA Tel.: 301 504 8416 Fax: 301 504 8414 Email: tats@lps1.barc.usda.gov Single pass sequencing. Bases called and alt.trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. PCR primers FORWARD: AGGAACAAGCATATGACCCT BACKWARD: GTTTTCCCACTCACGACG Plate: 121 row: M column: 18	

FEATURES		Seq primer: ATTAGTGCACATATAG.
source	Location/Qualifiers	
	1..564	
	/organism="Bos taurus"	
	/db_xref="taxon:9913"	
	/clone_1lb="BARC 5B0V"	
	/tissue_type="pooled"	
	/lab_host="DH10B"	
	/note="Vector: pCMV SPORT6; site_1: XbaI; site_2: XhoI; library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."	
BASE COUNT	106 a 191 c 155 g 112 t	
ORIGIN		

Query Match	76.9%	Score 256.2;	DB 10;	Length 564;
Best Local Similarity	85.6%;	Pred. NO. 2.4e-57;		
Matches 285; Conservative	0;	Mismatches 48;	Indels 0;	Gaps 0;

Oy	1	caaatgctgcgactcaacgctctctcgtctgtgtgtccctgggacgaaggtctcatc	60
Db	100	CAGGTGTGCTGACTCACCTCTCTCGTTCGGGTCCTGGGCCAGAGATTCATC	155
Oy	61	aactgctcttgaagaagcagcaacatttggagtaatcgtatgttggctgtgtacaaag	120
Db	160	ACCTGCTCTGTGAAGCAGCAGCAACATTGGAACTGGCAATTATGTGAGATTGTTCACAC	219
Oy	121	gtcccaagatcagcccccagactctctacagtgtctaaacggaatcgagctctggggtc	180
Db	220	ATCCAGGATGTGGCCCCGAGAACCTCTATCTAGGTTGCCACGATCGACCCAGGGGTC	279
Oy	181	cccgaccgaattcttcggtctccaggtctctggaaacagccacctgtaccatcagtctgc	240
Db	280	CCCGACCCATTTCTCCGGTCTCAGGCTCTGGGAACATAACCAACCTCGACATCTAGCTTCCTC	339
Oy	241	caggcttgaagacagagccgatattactgtgtcaatcgatacaaaatcactaagttgtgtc	300
Db	340	CAGGCTGAAGACGAGGCGAGATTAATTTCGTGTCATCTTATATCAGGTTGGTAGGACAGCTGT	399
Oy	301	ttcggcagcgggacccagagcttaccgtctcgtgtc	333
Db	400	TTTCGGCGCGGACTACTATTGACCTCTCTGGGT	432

RESULT	5				
LOCUS	BG691510				
DEFINITION	BG691510	655 bp	mRNA	linear	EST 02-MAY-2001
ACCESSION	340705 BARC	5BOV Bos taurus	CDNA 5',	mRNA sequence.	
VERSION	BG691510				
KEYWORDS	BG691510.1	GI:13933330			
SOURCE	EST.				
ORGANISM	Cow,				
	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
	Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 655)				
AUTHORS	Sonstegard,T.S., Capucio,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.				
TITLE	Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library				
JOURNAL	unpublished (2000)				
COMMENT	Contact: Sonstegard TS				
	USA, ARS, Beltsville Agricultural Research Center				
	Bldg. 200 Rm 2A, Beltsville, MD 20705, USA				
	Tel.: 301 504 8416				
	Fax: 301 504 8414				
	Email: tads@psi.barc.usda.gov				
	Single pass sequencing. Bases called and alt trimmed with phred				
	v0.980904.e. Vector identified by cross_match with the -m5score 18				
	and -mismatch 12 options.				
	PCR primers				

FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCCCGAGTCACGACG
 Plate: 99 row: 1 column: 6
 Seq primer: ATTTAGGTGACACTATAG.

FEATURES

Location/Qualifiers
 1. 655

BASE COUNT 129 a 221 c 181 g 124 t
 ORIGIN
 Query Match 75.4%; Score 251.2; DB 10; Length 655;
 Best Local Similarity 86.3%; Pred. No. 5.2e-56;
 Matches 290; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY 1 cagagatgtctgactcagccgctccctcgtctctggtgtcccttggccagaggtctccatc 60
 DB 88 CAGGCTGTGCTGACTCAGCGCTCCTCCGTGCGGGTCCTGGCCAGAGGGTCTCCATC 147
 QY 61 acctgtcttgaagcaagcaacaattggaagttaattgtatgtggctgtaccacaag 120
 DB 148 ACCGTCTGTGGAAGCAACAGCAATGTTGGAAGTGCATTTATGTGAGCTGTTCACACAG 207
 QY 121 gtccagagatcagcccccagactctctcatcagtggtctacaacagatcagacctcggggatc 180
 DB 208 ATCCAGAGATCGGCCCCCAAAATGCTCATCTATGATGTCGACACAGTCAAGCCTTGGGGTC 267
 QY 181 ccgagaccattctccggtctcaggtctcagtggtggaacaacagcccccagaccatcagctcgtc 240
 DB 268 CCCGACCGATTCTCCGGCTCAGAGTCTGGGAACACAGCCACCGTCACTACAGCTCCCTC 327
 QY 241 caggtctgaagcaagcgagatcttactgtgcatcgatata---aaatcttaccagtgtc 297
 DB 328 CAGGCCAGAGACGAGCGGATTTATTCTGTGCATCTCTGACACTATACAGAGAGTTT 387
 QY 298 gtttcggcagcgggaccaggtcagccgtctcgtgt 333
 DB 388 TTTTTCGGCAGCGGACACACACTGACCTGCTGGGT 423

RESULT 6

LOCUS BE590205 467 bp mRNA linear EST 28-AUG-2000
 DEFINITION 197215 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE590205
 VERSION BE590205.1 GI:9843244
 KEYWORDS EST.
 SOURCE
 ORGANISM Bos taurus
 Cow.
 Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 467)
 Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and

AUTHORS Wells,K.D.
 TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
 gland cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tadelspsi@ars.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.
 PCR Primers

FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCCCGAGTCACGACG
 Plate: 117 row: M column: 12
 Seq primer: ATTTAGGTGACACTATAG.

FEATURES

Location/Qualifiers
 1. 467

BASE COUNT 83 a 161 c 126 g 97 t
 ORIGIN
 Query Match 75.0%; Score 249.6; DB 10; Length 467;
 Best Local Similarity 86.0%; Pred. No. 1.2e-55;
 Matches 289; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 1 cagagatgtctgactcagccgctccctcgtctctggtgtcccttggccagaggtctccatc 60
 DB 74 CAGGCTGTGCTGACTCAGCGCTCCTCCGTGCGGGTCCTGGCCAGAGGGTCTCCATC 133
 QY 61 acctgtcttgaagcaagcaacaattggaagttaattgtatgtggctgtaccacaag 120
 DB 134 ACCGTCTGTGGAAGCAACAGCAATGTTGGAAGTGCATTTATGTGAGCTGTTCACACAG 193
 QY 121 gtccagagatcagcccccagactctctcatcagtggtctacaacagatcagacctcggggatc 180
 DB 194 ATCCAGAGATCGGCCCCCAAAATGCTCATCTATGATGTCGACACAGTCAAGCCTTGGGGTC 253
 QY 181 ccgagaccattctccggtctcaggtctcagtggtggaacaacagcccccagaccatcagctcgtc 240
 DB 254 CCCGACCGATTCTCCGGCTCAGAGTCTGGGAACACAGCCACCGTCACTACAGCTCCCTC 313
 QY 241 caggtctgaagcaagcgagatcttactgtgcatcgatataaagtactac---agtgtc 297
 DB 314 CAGGCCAGAGACGAGCGGATTTATTCTGTGCATCTCTGACACTATACAGAGAGTGT 373
 QY 298 gtttcggcagcgggaccaggtcagccgtctcgtgt 333
 DB 374 AGATTTCGGCAGCGGACACACACTGACCTGCTGGGT 409

RESULT 7

LOCUS BE487574 493 bp mRNA linear EST 28-AUG-2000
 DEFINITION 176397 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE487574
 VERSION BE487574.1 GI:9607107
 KEYWORDS EST.
 SOURCE
 ORGANISM Bos taurus
 Cow.
 Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 493)
 Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and

AUTHORS Wells,K.D.
 TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
 gland cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
Wells, K.D.

JOURNAL
gland cDNA library
Unpublished (2000)
COMMENT
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tadelpsi@barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 28 row: L column: 3
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1.496
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_11b="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

BASE COUNT 98 a 167 c 133 g 98 t
ORIGIN

Query Match 73.0%; Score 243.2; DB 10; Length 496;
Best Local Similarity 86.9%; Pred. No. 6e-54;
Matches 292; Conservative 0; Mismatches 38; Indels 6; Gaps 2;

QY 1 caggatgtctgctcagcgcgtctccgtgctgggtccctggcagagggtctcacc 60
|||||
DB 89 CAGGCTGTGTGATCAGCCATCATCGTGTCCGGGCTCCGCGACAGAGGCTCTCATC 148
QY 61 acctgtcttggaaagcagcaacattggaagtaatgtctatgtggctgtgtaccacag 120
|||||
DB 149 ACTGCTCTGGAAAGCAGCAGCATGTTGGA--AATGATATGTAGCTGTACCAACTG 205
QY 121 gtccagagatcagcccccagactccatcagtgctacaacgcgaltcgagcctcgggatc 180
|||||
DB 206 ATCCAGAGATCGGCGCCAGAACCTCATCTATGTGTGACACACAGTGGAGCCTCGGGGGTTC 265
QY 181 cccgacgattctccggtctccaggtcttggaaacacagccaccctgaccatcaactgcgc 240
|||||
DB 266 CCCGACCGATTCTCCGGCTCCAGGCTCTGGGAACACAGCCACCTGACCATCACTGCGCTC 325
QY 241 caggctgagagcagagccgattatctactgtcatcgtlatcaaaagtactaacag---tggt 297
|||||
DB 326 CAGGCTGAGAGCAGGACAGATTATTCTGTGCACTGTGCTAGAGATAGTACATAATAGCT 385
QY 298 gtcttcgagcgagcagcaggtcgaccgtcttggt 333
|||||
DB 386 GTTTTCGGCAGCGGACCACTGACGTCCTGGGT 421

RESULT 10
LOCUS BG689524 484 bp mRNA linear EST 02-MAY-2001
DEFINITION 337633 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BG689524
VERSION BG689524.1 GI:13931325
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 484)

AUTHORS
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
Wells, K.D.
TITLE
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tadelpsi@barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 102 row: K column: 2
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1.484
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_11b="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

BASE COUNT 86 a 161 c 136 g 101 t
ORIGIN

Query Match 72.1%; Score 240.2; DB 10; Length 484;
Best Local Similarity 82.6%; Pred. No. 3.7e-53;
Matches 275; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 caggatgtctgctcagcgcgtctccgtgctgggtccctggcagagggtctcacc 60
|||||
DB 93 CAGGCTGTGTGATCAGCCGCTCTCCGTGCTCCGGGCTCCGCGACAGAGGCTCTCATC 152
QY 61 acctgtcttggaaagcagcaacattggaagtaatgtctatgtggctgtgtaccacag 120
|||||
DB 153 ACTGCTCTGGAAAGCAGCAGCATGTTGGACTTGCAATGATGTGATTGCTTCCCAACAG 212
QY 121 gtccagagatcagcccccagactccatcagtgctacaacgcgaltcgagcctcgggatc 180
|||||
DB 213 ATCCAGAGATCGGCGCCAGAACCTCATCTATGTGTGCGACAGACACCTCTGGGGTTC 272
QY 181 cccgacgattctccggtctccaggtcttggaaacacagccaccctgaccatcaactgcgc 240
|||||
DB 273 CCCGACCGATTCTCCGGCTCCAGGCTCTGGGAACACAGCCACCTGACCATCACTGCGCTC 332
QY 241 caggctgagagcagagccgattatctactgtcatcgtlatcaaaagtactaacagtggtgt 300
|||||
DB 333 CAGGCCGAGAGCAGGCGGATTTATTTGTTCATCTCTGATAGTAGTAGGCGTGTGATT 392
QY 301 ttccgagcgagcagcagcaggtcgaccgtcttggt 333
|||||
DB 393 TTCCGCGCGCGGACCACTAAGCTGTGGGT 425

RESULT 11
LOCUS BE483566 518 bp mRNA linear EST 28-AUG-2000
DEFINITION 169766 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE483566
VERSION BE483566.1 GI:9603099
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 518)
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
Wells, K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAAT
BACKWARD: GTTTCCTGACGACGACG
Plate: 23 row: L column: 14
Seq primer: ATTGAGTGCACCTATG.
Location/Qualifiers
1. 518
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 580V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

BASE COUNT 101 a 177 c 141 g 99 t

ORIGIN

Query Match 72.1%; Score 240; DB 10; Length 518;
Best Local Similarity 86.3%; Pred. No. 4.3e-53;
Matches 290; Conservative 0; Mismatches 40; Indels 6; Gaps 2;

QY 1 caggatgtgtgactgactgacgcgtctccgtgctgctggtccctgggcccagaggtctccatc 60
|||||
DB 92 CAGGCTGTGCTGACTGACTGACCATCATCGTCCGGGCTCCCTGGGCGAGAGGCTCCATC 151
QY 61 acctgtcttggaaagcagcgaacattggaggttaagtctatgtggctgtgtaccaaag 120
|||||
DB 152 ACCTGACCGGAGGACGACCAATGTTGA--AATGGATATGTGACCTGTTCCAAACAG 208
QY 121 gtccaggaatcagccccagactccatcagtgctgactacaacgactcagcctcgggagtc 180
|||||
DB 209 ATCCGAGATCGGCCCCCGACCAACCTCATCTATGTGACACAGCTGAGGCTGGGGGTC 268
QY 181 cccgaccgattcttcggtctcaggtctggtggaacacagccacccctgacatcagctcgtc 240
|||||
DB 269 CCCGACGAGATTCTCCGGCTCCAGGTCTGGGAGACACGCCCTGACCATCAGCTCGCTC 328
QY 241 caggctgagagcagcgcgcatatctactgtgcatcgatataaagtacttcag--tggt 297
|||||
DB 329 CAGGCTGAGATGAGCAGATTATTTCTGTGAGCTGTGTACAGCACTAGCACTAATAGCT 388
QY 298 gtttcgagcgggagccagcgtcagcgtctcgtgt 333
|||||
DB 389 GTTTGGCAGCGGACCACTGACCGTCTGGGT 424

RESULT 12
LOCUS BE751028 542 bp mRNA linear EST 25-APR-2001
DEFINITION 202731 MARC 280V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE751028
VERSION BE751028.1 GI:10165020
KEYWORDS EST.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

cow.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 542)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., Laegreid, W.W., Cho, J., Fahrnenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko, McKown, C.G.,
Perla, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keeler, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAAT
BACKWARD: GTTTCCTGACGACGACG
Plate: 42 row: B column: 15
Seq primer: ATTGAGTGCACCTATG.
Location/Qualifiers
1. 542
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 280V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

BASE COUNT 102 a 183 c 144 g 112 t 1 others

ORIGIN

Query Match 71.9%; Score 239.4; DB 10; Length 542;
Best Local Similarity 86.2%; Pred. No. 6.3e-53;
Matches 288; Conservative 0; Mismatches 42; Indels 4; Gaps 2;

QY 1 caggatgtgtgactgactgacgcgtctccgtgctgctggtccctgggcccagaggtctccatc 60
|||||
DB 92 CAGGCTGTGCTGACTGACTGACCGCTCTCCGTGCTCCGGCTCCCTGGGCGAGAGGCTCCATC 151
QY 61 acctgtcttggaaagcagcgaacattggaggttaagtctatgtggctgtgtaccaaag 120
|||||
DB 152 ACCGCTCTGGAAGACACCAACAT--CGGTGATATGATGTGGCTGTACCAACAG 208
QY 121 gtccaggaatcagccccagactccatcagtgctgactacaacgactcagcctcgggagtc 180
|||||
DB 209 GTCCAGGATCGGCTCATATACCATCATCTATGTGTAGCACTGACCTCGGGGTC 268
QY 181 cccgaccgattcttcggtctcaggtctggtggaacacagccacccctgacatcagctcgtc 240
|||||
DB 269 CCCGACGAGATTCTCCGGCTCCAGTCTGGGAGACACAGCCCTGACCATCAGCTCGCTC 328
QY 241 caggctgagagcagcgcgcatatctactgtgcatcgatataaagtacttcagt-99tgt 299
|||||
DB 329 CAGGCTGAGATGAGCAGCGCATTTATTTCTGTGATGACTATGACAGTACTAGCACTAATAGT 388
QY 300 ttctggcagcgggagccagcgtcagcgtctcgtgt 333
|||||
DB 389 TTTGGCAGCGGACCACTGACCGTCTGGGT 422

RESULT 13
 BE722165 557 bp mRNA linear EST 25-Apr-2001
 LOCUS 190280 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BE722165
 ACCESSION BE722165
 VERSION BE722165.1 GI:10123461
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 557)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
 Petta,G., Holt,I., Karayancheva,S., Liang,F., Quackenbush,J. and
 Keeler,J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 JOURNAL libraries and construction of a gene index for cattle
 MEDLINE Genome Res. 11 (4), 626-630 (2001)
 COMMENT 21180013
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mnscore 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACGTCACGACG
 Plate: 102 row: L column: 3
 Seq primer: ATTAGTGACTATAG.
 Location/Qualifiers
 1..557
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 4BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from day 20 and day 40
 embryos."

BASE COUNT 115 a 175 c 142 g 125 t
 ORIGIN

Query Match 71.4%; Score 237.6; DB 10; Length 557;
 Best Local Similarity 88.4%; Pred. No. 1.9e-52;
 Matches 258; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 cagatgtgtgactacgcgcgtctccgtgtctgtgtgtgtccctggcgcaagaggtctcatc 60
 DB 89 CAGGCTGTGTGACTCAGCCGCTCCTCGTGTCCGGTCCCTGGGCGAGAGGCTCTCATC 148
 QY 61 acctgctctggaacagcaacaattggaagttaattgtatgtgtgtgtgtacacag 120
 DB 149 ACAGGCTCTGTGAACACAGCAGCATGTTGATATGCAATTAATGTGACCTGTTCCAAAG 208
 QY 121 gtccagagatcagcccccagactcctcatcagtgctacaacagatcgagctcgagatc 180
 DB 209 ATCCAGAGATCGGCCCCACAGACCTCATATGTTGATGACACACATCGACGCTCGGGGCTC 268
 QY 181 ccgagaccgattctcgggtccaggtctgtggaacacagcaaccctgaccatcagctgc 240
 DB 269 CCCGACCGATTCTCCGGCTCCAGGTCTGGGAACACAGCCCGACCATCAGCTCGCTC 328
 QY 241 caggctagagagagcgccgatttactgtgcatcgatataaagtlacttaca 292
 DB 329 CAGGCTGAGGACGAGGAGATTATTCTGTGCATCTTATCAGAGTGTAAACA 380

RESULT 14
 BE485929 503 bp mRNA linear EST 28-AUG-2000
 LOCUS 173232 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BE485929
 ACCESSION BE485929
 VERSION BE485929.1 GI:9605462
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 503)
 Sonstegard,T.S., Capuco,A.V., Van Tassel,L.C.P., Ashwell,M.S. and
 Wells,K.D.
 TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
 JOURNAL gland cDNA library
 COMMENT Unpublished (2000)
 Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@ps1.barc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mnscore 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACGTCACGACG
 Plate: 131 row: H column: 15
 Seq primer: ATTAGTGACTATAG.
 Location/Qualifiers
 1..503
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BARC 5BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

BASE COUNT 92 a 175 c 134 g 102 t
 ORIGIN

Query Match 71.1%; Score 236.8; DB 10; Length 503;
 Best Local Similarity 85.7%; Pred. No. 3e-52;
 Matches 288; Conservative 0; Mismatches 42; Indels 6; Gaps 2;

QY 1 cagatgtgtgactacgcgcgtctccgtgtctgtgtgtgtccctggcgcaagaggtctcatc 60
 DB 89 CAGGCTGTGTGACTCAGCCGCTCCTCGTGTCCGGTCCCTGGGCGAGAGGCTCTCATC 148
 QY 61 acctgctctggaacagcaacaattggaagttaattgtatgtgtgtgtgtacacag 120
 DB 149 ACCTGCTCTGTGAACACAGCAGCATGTTGATATGCAATTAATGTGACCTGTTCCAAAG 205
 QY 121 gtccagagatcagcccccagactcctcatcagtgctacaacagatcgagctcgagatc 180
 DB 206 GTCCAGAGATCGGCCCCACAGACCATCATATGTTGATGACAGTGCACCTCGGGGCTC 265
 QY 181 ccgagaccgattctcgggtccaggtctgtggaacacagcaaccctgaccatcagctgc 240
 DB 266 CCCGACCGATTCTCCGGCTCCAGGTCTGGGAACACAGCCCGACCATCAGCTCGCTC 325
 QY 241 caggctagagagagcgccgatttactgtgcatcgatataaagtlacttaca 297
 DB 326 CAGGCTGAGGACGAGGAGATTATTCTGTGTGACTTATGACAGTGTAAACA 385

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 22:10:19 ; Search time 376.54 Seconds
(without alignments)
1518.385 Million cell updates/sec

Title: US-09-786-015-3

Perfect score: 333

Sequence: 1 cagagctgctgactcagcc.....ccagctgacgcctcgtggt 333

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	333	21	AAA08401
2	206.2	61.9	331	22	AA168771
3	198.4	59.6	335	22	AAC66525
4	197	59.2	339	22	AAH47733
5	195.4	58.7	385	22	AA158663
6	193.6	58.1	738	21	AA255614
7	193.2	58.0	348	22	AAH74666
8	193.2	58.0	915	22	AAH74670
9	193.2	58.0	22	AAH74679	

10	193	58.0	330	22	AA503520
11	192.2	57.7	628	14	AA036134
12	192.2	57.7	891	22	AAC66528
13	192.2	57.7	1044	12	AAQ12840
14	190.2	57.1	464	22	AAE92354
15	189.6	56.9	333	22	AAH42401
16	189.6	56.9	333	22	AAH42407
17	189.6	56.9	351	22	AA168765
18	189	56.8	330	21	AAA27661
19	189	56.8	482	21	AAC98409
20	188.2	56.5	330	22	AAS03477
21	187.4	56.3	390	19	AAV33307
22	187.4	56.3	747	21	AA678668
23	187.4	56.3	889	23	AA577073
24	187.4	56.3	9071	13	AAQ22491
25	187.4	56.3	9071	13	AAQ23370
26	187.2	56.2	393	18	AAE80759
27	187.2	56.2	933	20	AAV72534
28	186.4	56.0	351	22	AA168755
29	185.8	55.8	333	17	AAE10327
30	185.8	55.8	333	17	AA231655
31	185.8	55.8	756	23	AAS83477
32	185.8	55.8	866	23	AAS87037
33	185.6	55.7	393	18	AAE72648
34	185.6	55.7	774	18	AAE50787
35	184.2	55.3	333	20	AA231654
36	184	55.3	336	21	AAC96953
37	184	55.3	342	24	ABA94217
38	184	55.3	884	11	AAQ03609
39	182.8	54.9	333	20	AAV72226
40	182.4	54.8	334	22	AAH47514
41	182.4	54.8	342	24	ABA94244
42	182.2	54.7	330	11	AAQ03607
43	182	54.7	330	22	AAH68677
44	182	54.7	732	20	AAH86940
45	182	54.7	732	20	AAH86941

ALIGNMENTS

RESULT 1
AAA08401
ID AAA08401 standard; DNA; 333 BP.
XX
AC AAA08401;
XX
XX
XX 13-JUL-2000 (first entry)
XX
XX Carcinoembryonic antigen affinity antibody light chain variable region.
XX
XX
XX Carcinoembryonic antigen; CEA; sheep; monoclonal antibody;
XX
XX tumour associated antigen; anti-carcinogenic; cytostatic;
XX
XX cancer therapy; ds.
XX
XX Ovis sp.
XX
XX WO200012556-A1.
XX
XX 09-MAR-2000.
XX
XX 20-AUG-1999; 99MO-CB02729.
XX
XX PF
XX 28-AUG-1998; 98GB-0018915.
XX
XX (KSBI-) KS BIOMEDIX LTD.
XX
XX Harrison FU;
XX
XX WPI; 2000-375618/32.
XX
XX P-PSDB; AAH82529.
XX
XX A new high-affinity monoclonal antibody that is characterized by an

DNA encoding anti-M4H7 MAb light ch
Human immune syste
Variable region of
Bovine mammary tis
Nucleotide sequenc
Nucleotide sequenc
Human autoantibody
DNA encoding anti-
Human colon cancer
DNA encoding anti-
Anti-human CD23 6G
Recombinant human
DNA encoding novel
Human U266 lambda
U266-lambda gene a
64-863 antibody HS
Single chain Apo-2
Human autoantibody
Human anti-Pseudom
Coding sequence fo
DNA encoding novel
DNA encoding novel
HSV 863 antibody 1
C6 human sfv antib
Coding sequence fo
Human anti-HBs ant
shgM22 light chai
Sequence encoding
Human anti-gep1b/I
Anti-IL-18 antibod
shgM22 light chai
Sequence encoding
Human anti-Rh(D) c
Antibody B10A8 enc
Antibody B10A8 com

PT acid-washed enzyme-linked immunosorbent assay for use in cancer therapy
XX
PS
XX Claim 9; Page 15; 21pp; English.
XX
CC The present invention describes a high-affinity monoclonal antibody
CC characterised by an acid-washed enzyme-linked immunosorbent assay (EIA).
CC The antibody is used in cancer therapy. Association of the new antibody
CC with an antigen is favoured over dissociation in vivo and they therefore
CC have longer localisation times at target sites, resulting in a higher
CC concentration of antibodies localised at the target sites. Targeting the
CC antibody to a site in vivo is improved. The concentration of antibody
CC does not need to be too high which reduces side-effects and costs of
CC therapy. The present sequence encodes the light chain variable region
CC of a monoclonal antibody having affinity for carcinoembryonic antigen
CC (CEA, a tumour associated antigen), which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 333 BP; 66 A; 103 C; 94 G; 70 T; 0 other;

Query Match 100.0%; Score 333; DB 21; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.9e-86;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagagatgctgactcaagccgctccgtgctggtccctggcgccagaggtccatc 60
DB 1 cagagatgctgactcaagccgctccgtgctggtccctggcgccagaggtccatc 60
QY 61 acctctctcggaagcagcagcaacttgaggtatgctatgctggcgctgtaaccaag 120
DB 61 acctctctcggaagcagcagcaacttgaggtatgctatgctggcgctgtaaccaag 120
QY 121 gtccagagatcagcccccagactcctcatcagtgctacaaacagatcgactcgaggatc 180
DB 121 gtccagagatcagcccccagactcctcatcagtgctacaaacagatcgactcgaggatc 180
QY 181 cccgacagatctccggtccaggtctggaacacagccacctgacctgctgcgc 240
DB 181 cccgacagatctccggtccaggtctggaacacagccacctgacctgctgcgc 240
QY 241 caggtctgaggaagcagcagatattactgtgcatcgatcaagaagtactacagtgtgt 300
DB 241 caggtctgaggaagcagcagatattactgtgcatcgatcaagaagtactacagtgtgt 300
QY 301 ttcggcagcgagcagcaggtctgacctgtggt 333
DB 301 ttcggcagcgagcagcaggtctgacctgtggt 333

RESULT 2
AAI68771
ID AAI68771 standard; DNA; 331 BP.
AC AAI68771;
XX
DT 22-JAN-2002 (first entry)
XX
DE Human autoantibody MICA-10 variable region heavy chain DNA.
XX
KW Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;
KW glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;
KW polyglutandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;
KW variable region; heavy chain; MICA-10; ds.
XX
OS Homo sapiens.
XX
PN EP1149914-A2.
XX
PD 31-OCT-2001.
XX
PF 29-MAR-2001; 2001EP-0107702.
XX
PR 10-APR-2000; 2000DE-1017782.

PR 25-MAY-2000; 2000DE-1025840.
XX
PA (LABO-) LABOR KOCH MERK GMBH.
XX
PI Richter W, Rickert M, Rapp I, Dangel W;
XX
DR WPI; 2001-640702/74.
XX
P-PSDB; AAG80222.
XX
PS New fusion protein, useful for diagnosis of diabetes type I and other
PT metabolic diseases, is reactive with autoantibodies against both
PT glutamate decarboxylase and islet cell antigen
XX
XX Disclosure; Page 40-41; 68pp; German.
XX
CC This invention describes a novel fusion protein (I) that has, at its
CC N-terminus, one or more epitopes that bind specifically to autoantibodies
CC (AAb) against the islet cell antigen IA2 and, at its C-terminus, one or
CC more epitopes that bind specifically to antibodies (Ab) directed against
CC the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding
CC it, vectors containing (II) and transformed cells, are useful for
CC diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,
CC polyglutandular autoimmune syndrome or other autoimmune conditions
CC associated with AAb against GAD65 or IA2. (I) provides a rapid and simple
CC diagnosis of high specificity and sensitivity, capable of recognizing
CC antibodies against both IA2 and GAD65, simultaneously. Unlike known
CC fusions, where the GAD65 component is at the N-terminus, (I) contains
CC correctly folded conformational epitopes that can react with most MICA
CC autoantibodies. This sequence encodes the human autoantibody MICA-10
CC variable region heavy chain used in the method of the invention.
XX
SQ Sequence 331 BP; 66 A; 106 C; 91 G; 68 T; 0 other;

Query Match 61.9%; Score 206.2; DB 22; Length 331;
Best Local Similarity 76.4%; Pred. No. 8.8e-50;
Matches 253; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1 cagagatgctgactcaagccgctccgtgctggtccctggcgccagaggtccatc 60
DB 1 cagctctgtgtgactcaagccgctccgtgctggtccctggcgccagaggtccatc 60
QY 61 acctctctcggaagcagcagcaacttgaggtatgctatgctggcgctgtaaccaag 120
DB 61 acctctctcggaagcagcagcaacttgaggtatgctatgctggcgctgtaaccaag 120
QY 121 gtccagagatcagcccccagactcctcatcagtgctacaaacagatcgactcgaggatc 180
DB 121 cttccagagatcagcccccagactcctcatcagtgctacaaacagatcgactcgaggatc 180
QY 181 cccgacagatctccggtccaggtctggaacacagccacctgacctgactgcgc 240
DB 181 cctgacagatctctcggtccaggtctggaacacagccacctgacctgactgcgc 240
QY 241 caggtctgaggaagcagcagatattactgtgcatcgatcaagaagtactacagtgtgt 300
DB 241 caggtctgaggaagcagcagatattactgtgcatcgatcaagaagtactacagtgtgt 300
QY 301 ttcggcagcgagcagcaggtctgacctgtggt 331
DB 301 ttcggcagcgagcagcaggtctgacctgtggt 331

RESULT 3
AAC66525
ID AAC66525 standard; CDNA; 935 BP.
AC AAC66525;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-7 coding sequence.
XX

XX	AA158663	standard; cDNA; 585 BP.
ID	AA158663	standard; cDNA; 585 BP.
AC	AA158663	
XX	AA158663	
DT	22-OCT-2001	(first entry)
XX	22-OCT-2001	(first entry)
DE	Human polynucleotide SEQ ID NO 866.	
XX	Human polynucleotide SEQ ID NO 866.	
KW	Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;	
KW	peripheral nervous system; neurophy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;	
KW	leukaemia; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	MO20015312-A1.	
PN	MO20015312-A1.	
XX	26-JUL-2001.	
PD	26-JUL-2001.	
XX	26-JUL-2001.	
XX	26-DEC-2000; 2000WO-US34263.	
PE	26-DEC-2000; 2000WO-US34263.	
XX	21-JAN-2000; 2000US-0486725.	
PR	21-JAN-2000; 2000US-0486725.	
PR	25-APR-2000; 2000US-0552317.	
PR	09-JUL-2000; 2000US-0596042.	
PR	19-JUL-2000; 2000US-0620312.	
PR	03-AUG-2000; 2000US-0653450.	
PR	14-SEP-2000; 2000US-0662191.	
PR	19-OCT-2000; 2000US-0693036.	
PR	29-NOV-2000; 2000US-0727344.	
XX	(HYSE-) HYSEQ INC.	
PA	(HYSE-) HYSEQ INC.	
XX	Tang Y T, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;	
PI	Zhao QAI, Zhou P, Goodrich R, Dimaac RT;	
XX	WPI: 2001-442253/47.	
DR	P-PSDB; AAM39507.	
XX	Novel nucleic acids and polypeptides, useful for treating disorders	
XX	such as central nervous system injuries -	
PT	Claim 1; SEQ ID NO 866; 10078bp; English.	
PS	Claim 1; SEQ ID NO 866; 10078bp; English.	
XX	The invention relates to human nucleic acids (AA157798-AA161369) and	
CC	the encoded polypeptides (AAM38642-AAM42213) with nootropic,	
CC	immunosuppressant and cyostatic activity. The polynucleotides are useful	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide	
CC	of the invention may be used to treat diseases of the peripheral nervous	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and	
CC	localised neuropathies and central nervous system diseases, such as	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	
CC	utilisation of the activities such as: immune system suppression,	
CC	Activin/Inhibin activity, chemotactic/chemokine activity, haemostatic	
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,	
CC	assays for receptor activity, arthritis and inflammation, leukaemias and	
CC	C.N.S disorders.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification.	
XX	Sequence 585 BP; 113 A; 194 C; 156 G; 122 T; 0 other;	
XX	Sequence 585 BP; 113 A; 194 C; 156 G; 122 T; 0 other;	

	Query Match	58.7%	Score 195.4	DB 22	Length 585
	Best Local Similarity	75.8%	Pred. No. 1.3e-46		
	Matches 257	Conservative 0	Mismatches 76	Indels 6	Gaps 1
QY	1	cagagtgcgtacccacgcgcgtccctcggtctgtgtccctcgccacagaggtccacc	60		

Db	124	cagctctgtcgtgaagcagccgcctcagtgctctggggcccagggcagaaggggtaccatc	183
Qy	61	acctgctctggaaacagacagcaaatgtgagatgaatgctatgtggctggtaccacag	120
Db	184	tctctgactgggagcagctccaatcctcagatcggggatgatgatgtacctgtaccacga	243
Qy	121	gtcccaagatcagcccccaagactcctcatcagtgtctaacacgcatcgagcttcgggac	180
Db	244	cttcacaggaacagcccccaactcctcatctatgtatgtaacagcaatcggcctcgaagg	303
Qy	181	cccgacacatctccggtccaggtctcgggaaacagacccctgacacatcagctgc	240
Db	304	ctgaacgcatctctgtgctccaaagtctcggacactcagcctcccttgccatcaatggtcc	363
Qy	241	caggctgagagcagagccgcatcttactgtgcatcgtatcaagtacttaacagtgt---	297
Db	364	cagctgagagtgatggctgtgattactgtcagcttcactgaacagcagcctgagtggtct	423
Qy	298	---gtttcggcagcgggaccagcgtgacgcgttcgtgt 333	
Db	424	gtggtatcggcggagagaccagctgacgcgtcaggt 462	
RESULT 6			
AA255614			
ID	AA255614	standard; cDNA; 738 BP.	
XX	AA255614;		
XX	27-MAR-2000	(first entry)	
XX			
DE	Internalising anti-c-erbB-2 receptor antibody scFv F5 cDNA.		
XX			
KW	Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;		
XX	HER/neu oncogene; tumour-specific; internalisation; non-immunogenic; ss.		
XX			
OS	Synthetic.		
XX	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	mat_peptide	1..738	
FT		/*tag= a	
FT		/product= "Internalising anti-c-erbB-2 antibody F5"	
XX			
PN	W09955367-A1.		
XX			
PD	04-NOV-1999.		
XX			
PF	23-APR-1999;	99WO-US07395.	
XX			
PR	24-APR-1998;	98US-0082953.	
PR	12-FEB-1999;	99US-0250056.	
XX			
PPA	(REGC) UNIV CALIFORNIA.		
XX			
PI	Marks JD, Poul MA;		
XX			
DR	WPI; 2000-072168/06.		
XX			
DR	P-PSDB; AAY58235.		
XX			
PT	Novel internalizing antibodies used to treat cancer cells -		
XX			
PS	Claim 45; Page 81; 85pp; English.		
XX			
CC	This sequence represents cDNA encoding an internalising humanised		
CC	antibody, scFv F5, which specifically binds to the extracellular domain		
CC	of the c-erbB-2 receptor, the protein product of the HER/neu oncogene.		
CC	The scFv F5 antibody binds to the epitope of the c-erbB-2 receptor that		
CC	is bound by F5 antibodies. On binding the c-erbB-2 receptor, the		
CC	antibody is transported into the cell. The c-erbB-2 receptor is a marker		
CC	protein which is overexpressed by 30-50% of breast carcinomas and other		
CC	adenocarcinomas, and thus provides a useful cell surface marker for		
CC	specifically targeting tumour cells. The antibodies of the invention		

are used as tumour-targeting molecules for diagnosis and treatment. The antibodies can be attached to effector molecules. The effector molecules may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin; radionuclides; ligands such as growth factors; therapeutic agents such as vinblastine, vindesine or melphalan; ribozymes; or antisense molecules. The antibodies may also be used in vivo or in vitro for detection and/or quantitation of the c-erb-2 receptor and thus diagnosis and/or localisation of cancers characterised by expression of c-erb-2. Although antibodies have previously been used to target tumour cells, their success has been limited. The utility of prior art antibodies has been hampered by the paucity of tumour specific antibodies, antibody immunogenicity, low binding affinity, and poor tumour penetration. Immunogenicity could be avoided and toxicity reduced if high affinity tumour specific human antibodies were available. However, the production of human monoclonal antibodies using conventional hybridoma technology has proven difficult. Also, most of the antibodies produced react with antigens that are also common to non-malignant cells, which makes them unsuitable for use as tumour-targeting molecules. The antibodies of the invention overcome these difficulties, as they are targeted to a tumour-specific antigen, and avoid the problem of immunogenicity as they are human in origin.

SQ sequence 738 BP; 145 A; 204 C; 232 G; 157 T; 0 other;

Query match	58.18;	Score 193.6;	DB 21;	Length 738;
-------------	--------	--------------	--------	-------------

Matches 254; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

OY	1	caggatgctgctgactcaagccgctctccgctctctctgagccctctggccagaaaggtccatc	60
Db	403	cagctctgctgtagcagcagccgcccctcaagtctctggggcccacagggctcaacatc	462
OY	61	acctgctctctggaagcagcagcagaacatctgtaggttaatgctatctggtctgtgtaaccaag	120
Db	463	tccgcacctgggaacagactcccaacatctggggcaggttatgctgtgtaacctgtgtaaccag	522
OY	121	gtcccaagatcagccccccagacatcctcatcaagtctcaacacagctcagcctctgggatac	180
Db	523	cttcacgaaacagcccccaaacatctctatctatgctgttaaccacaaatcgggccctcaagggtc	582
OY	181	cccgaaacgcatctctcggctctccaaagttctctgggaacaacagccaacccatgaacatcgcgtc	240
Db	583	ctctaacgcatctctctgctctcaaaatctcgggaacatccacccctccctgccaatcaatctgctc	642
OY	241	caggctagagacagggccgcatattactctgtgcatcgtatcaagaagttaacttaagttgt---	297
Db	643	caggctcgtagagtagtgctgtattatctatctgcgaattcatgatacagcagccctgaagtgttg	702
OY	298	gttttcggcagcgggaccagagctgacccgctcctggt	333
Db	703	gtgtctcggcggagggacaaagcttaacggtctcagtt	738

RESULT	7
AAH74666	
ID	AAH74666 standard; DNA; 348 BP.

AC AAH74666;

DT 29-OCT-2001 (first entry)

DE Nucleotide sequence of the L chain variable region of SCFv1-4.

KM Complementarity determining region; CDR, single chain antibody; ScFv,
KM hepatitis C virus; HCV, HCV infection; CD81, E2 protein; NS1 protein,
KM envelope glycoprotein; ss.

OS Homo sapiens.

PN WO200158459-A1.

PD 16-AUG-2001.

XX	13-FEB-2001; 2001WO-JP00967.
PF	
XX	
PR	14-FEB-2000; 2000JP-0034906.

PA (MITS-) MITSUBISHI-TOKYO PHARM INC.

PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;

DR WPI; 2001-496986/54.

DR P-PSDB; AAG63630.

PT Remedies for hepatitis C containing substances with antiviral effects
PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT compounds, by inhibiting binding of hepatitis C virus envelope

PS Claim 40; Page 82-83; 138pp; Japanese.

CC The present sequence encodes the L chain variable region of a single
CC chain antibody of the invention. The specification describes a substance
CC can inhibit the binding between hepatitis C virus (HCV) and cells with
CC potential HCV infection, cells with expression of CD81, or CD81. Thus
CC substance is especially an antibody with affinity towards HCV E2/NS1
CC protein, containing amino acid sequences based on the complementarity
CC determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable
CC regions. The antibody inhibits the viral envelope glycoprotein. It is
CC also a CD81 inhibitor. The antibodies and drugs are used for treatment
CC and/or prevention of hepatitis C, or for diagnosis of hepatitis C.

Sequence 348 BP; 72 A; 109 C; 97 G; 70 T; 0 other;

Query Match	58.0%;	Score 193.2;	DB 22;	Length 348;
Best Local Similarity	75.5%;	Pred. No. 4.9e-46;		
Matches 240;	Conservative 0;	Mismatches 78;	Indels 0;	Gaps 0

Qy	1	cagatgctgctgactcaagccgctctccgctgtctgtgtgtcccttgagccagagagctctatc	60
Db	1	cagctctctgctcaactcaacgctctctctcagctgtctgtgtgtcccccaagcagaggtctacacata	60
Qy	61	acctgtctctgaaagcagagagaaacattggaagtaatgtcttaattgtgtctgtatccacaag	120
Db	61	tctgtcactgtgagcaggtctccacactcgggtcaggtatgtatgtatcactgtgtaccagag	120
Qy	121	gtcccaagataagccccagagctctcatcaaggtgtctcaacgatacgtacgtcttgaggatc	180
Db	121	cttccaaagaaacagcccccaaacctctcatctatctatctgaatacaacatctgcctcttaagggctc	180
Qy	181	cccgacagatctctccggtctcccaaggtctctggaagaaacagaccacccctgaaacatctgcgtc	240
Db	181	ctgtacagcatctctgtgtctcccaaggtctctgcacccctcagcctccctgtgcatacattgtgctc	240
Qy	241	caggtctgagagacgggcccgaattatctatctgtgactcgtatcaagaagtactcaatgttgtt	300
Db	241	caggtctgagaggtgtggtcgtatattactctgtccaggtccatctgaacagccctgaatgtgttt	300
Qy	301	tctgcgcagcgggaccagag	318
Db	301	gaggtctctgcgaaccggg	318

RESULT	8
AAH74670	
ID	AAH74670 standard; DNA; 915 BP.

AC AAH74670;

DT 29-OCT-2001 (first entry)

DE Nucleotide sequence of single chain antibody ScFv1-4.

KW Complementarity determining region; CDR; single chain antibody; ScFv;


```
QY 241 cagcgtcggagcagcgcgattactctgcatcgatcaagaagtactcaagtgtgtt 300
DB 736 cagcgcgaggaatgagcgtcttactctcagctcctaatagcagcgcctgagtggtt 795
QY 301 ttcgcgcagcgggagccagg 318
DB 796 gaggtcttcggaaccggg 813

RESULT 10
AA03520
ID AAS03520 standard; cDNA: 330 BP.
XX
AC AAS03520;
XX
DT 29-AUG-2001 (first entry)
XX
DE DNA encoding anti-adipocyte monoclonal antibody light chain, FAT 106.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
KW heart disease; complementarity determining region; CDR; ss.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB03900.
XX
PR 12-OCT-1999; 99US-0158812.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI: 2001-282031/29.
XX
P-PSDB: AAU02620.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity
PT related diseases -
XX
PS Disclosure: Page 167; 182pp; English.
XX
CC AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy
CC and light chain coding sequences of the invention. The antibodies can be
CC used in the treatment of obesity and obesity related diseases. The
CC antibodies can be used to deliver drugs or pro-drugs directly to the fat
CC mass of an obese patient or the antibody can be used as a therapeutic
CC itself. Antibodies binding specifically to adipocytes can be used to
CC activate the immune system to destroy the cells by complement mediated
CC lysis. The antibodies may be labeled with a detectable label such as
CC radiolabel, fluorescent or chemical group and used in methods of
CC diagnosis in human subjects e.g. to determine the presence of adipocyte
CC antigen on the surface of an adipocyte to detect or determine the
CC presence or level of adipocytes in a cell or tissue sample. The
CC antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.
XX
SQ Sequence 330 BP; 69 A; 101 C; 83 G; 77 T; 0 other;

Query Match 58.0%; Score 193; DB 22; Length 330;
Best Local Similarity 74.2%; Pred. No. 5, 5e-46;
Matches 244; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
```

```
QY 61 acctgctctggaagcagcagcaacattgaggtatgtctatctgtggtgtgtaccacag 120
DB 61 tcttgaccttggaacccagcagctggtgtgtatataactatgtcttctgtgtaccacag 120
QY 121 gtcccaagatcacgcccacagctccatcagtgctacaaccgatacagcctcgaggatc 180
DB 121 caccacaggaagcaccacacacatcatgattatgaggtacataaagcgcctccaggggtc 180
QY 181 cccgaccgattctccggtccaggtctggaacacagccaccctgaccatcagctgc 240
DB 181 cctgatcgtctctctgctcccaagctcgcaacacagctccctcgaccgtctcagactc 240
QY 241 cagcgtgagcagcagcgcgattactctgcatcgatcataaagtactcaagtgtgtt 300
DB 241 cagcgtgaggtatgagctgattactctgcatcattatgcaggaagcagcagcagtggtt 300
QY 301 ttcgcgcagcggaccagcgcgcgcctc 329
DB 301 ttcgcgcgagggagcaccagctgaccgtctc 329

RESULT 11
AA036134
ID AA036134 standard; DNA: 628 BP.
XX
AC AA036134;
XX
DT 25-MAY-1993 (first entry)
XX
DE MH4H7 MAb light chain coding sequence.
XX
KW Human; light chain; recombinant; monoclonal; antibody; MAb; MH4H7;
KW Nematelwa; microbial infection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH CDS 105..610
FT /*tag= a
FT 105..152
FT /*tag= b
FT /*number= Exon 1
FT 153..266
FT /*tag= c
FT /*number= Intron 1
FT 267..610
FT /*tag= d
FT /*number= Exon 2
XX
PN JP04360696-A.
XX
PD 14-DEC-1992.
XX
PF 06-JUN-1991; 91JP-0163886.
XX
PR 06-JUN-1991; 91JP-0163886.
XX
PA (SUMO ) SUMITOMO CHEM CO LTD.
PA (SUMO ) SUMITOMO SEIYAKU KK.
XX
DR WPI: 1993-032623/04.
XX
P-PSDB: AAR31535.
XX
DT Recombinant human antibody - produced using new human B
DT lymphocyte strain as the host
XX
PS Claim 5; Fig 9; 27pp; Japanese.
XX
CC This sequence encodes the light chain of a recombinant human
CC monoclonal antibody (MAb) designated MH4H7. This sequence was
CC introduced in to a Nematelwa cell strain which was cultured. The
CC MAb may be used in a drug for the prevention and treatment of
```

CC diseases caused by microbial infection.

XX Sequence 628 BP; 109 A; 202 C; 170 G; 147 T; 0 other;

Query Match 57.7%; Score 192.2; DB 14; Length 628;
Best Local Similarity 73.6%; Pred. No. 1.1e-45;
Matches 245; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```
QY 1 cagagatgtgtgactcagccgctccgtgtctgtctgtccctggccagaggtctccatc 60
    ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 cagctcgtccgtgactcagctcgtcgtctgtctgtctgtccctggccaggtcgtccatc 337
QY 61 acctgtcttgaagcagcagcaacattggagtaattgtatgttggctgtgtaccacag 120
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 tctgtacctgtgaaccagcagtgacattgtgtatataactatgtctctcgtgtaccacaa 397
QY 121 gtccagagatcagcccccagctccatcattagtggtataacagcagatcgagctcggggatc 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 caccacagcaaaccccccagctcgtatgtatgtctgtcagtaatcggccctcagggggt 457
QY 181 cccgacagatctcgcgctccaggtctcgtggacaacacacacccctgaccatcagctcgc 240
    | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 tctcatcgtctctcgtcgtcctcaagctcgtgcaacacagcgcctccctgaccatcctcgggctc 517
QY 241 caggtctgagagcagcagcagattactgtgcacgtatcacaagttacttaacagtgtgt 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 518 caggtctgagagcagcagcagattactgtgcacgtatcacaagttacttaacagtgtgt 577
QY 301 ttccgacgagcagcagcagcgtcgtcgtcgtgt 333
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 578 ttccgacgagagcagcagcgtcgtcgtcgtgt 610
```

RESULT 12

AAC6528
ID AAC6528 standard; cDNA; 891 BP.

AC AAC6528;

DT 15-FEB-2001 (first entry)

XX Human immune system associated protein HISAP-10 coding sequence.

XX Human; immune system associated protein; HISAP-10; immune disorder;

KW infection; autoimmune disease; cancer; ss.

XX Homo sapiens.

PN US6135941-A.

PD 24-OCT-2000.

PF 27-MAR-1998; 98US-0049672.

PR 27-MAR-1998; 98US-0049672.

PA (INCY-) INCYTE PHARM INC.

XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;

PI Hillman JL, Au-Young J;

DR WPI; 2001-030926/04.

DR P-PDB; AAB63212.

XX New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing
PT immune or cell proliferative disorders or infections -

XX Claim 3; Column 87-90; 54pp; English.

XX The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be

CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer.

XX Sequence 891 BP; 207 A; 287 C; 222 G; 175 T; 0 other;

Query Match 57.7%; Score 192.2; DB 22; Length 891;
Best Local Similarity 73.6%; Pred. No. 1.2e-45;
Matches 245; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```
QY 1 cagagatgtgtgactcagccgctccgtgtctgtctgtccctggccagaggtctccatc 60
    ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 cagctcgtccgtgactcagctcgtcgtctgtctgtctgtccctggccaggtcgtccatc 150
QY 61 acctgtcttgaagcagcagcaacattggagtaattgtatgttggctgtgtaccacag 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 tctgtacctgtgaaccagcagtgacattgtgtatataactatgtctctcgtgtaccacag 210
QY 121 gtccagagatcagcccccagctccatcattagtggtataacagcagatcgagctcggggatc 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 tcccccagcagcccccagctcgtatgtatgtcagtaatcggccctcagggggt 270
QY 181 cccgacagatctcgcgctccaggtctcgtggacaacacacacccctgaccatcagctcgc 240
    | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 271 tctcatcgtctctcgtcgtcctcaagctcgtgcaacacagcgcctccctgaccatcctcgggctc 330
QY 241 caggtctgagagcagcagcagattactgtgcacgtatcacaagttacttaacagtgtgt 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 331 caggtctgagagcagcagcagattactgtgcacgtatcacaagttacttaacagtgtgt 390
QY 301 ttccgacgagcagcagcagcgtcgtcgtcgtgt 333
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 391 ttccgacgagagcagcagcgtcgtcgtcgtgt 423
```

RESULT 13

AAQ12840
ID AAQ12840 standard; DNA; 1044 BP.

AC AAQ12840;

DT 17-OCT-1991 (first entry)

XX Variable region of lambda type light chain specific for LPS of

DE Pseudomonas aeruginosa.

XX Monoclonal antibody; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 562..892

FT /*tag= a

FT /label= LH

PN JP03151876-A.

XX 28-JUN-1991.

PF 08-NOV-1989; 89JP-0291981.

PR 08-NOV-1989; 89JP-0291981.

PA (SUMO) SUMITOMO CHEM IND KK.

DR WPI; 1991-234064/32.

DR P-PDB; AAR13184.

Query Match	57.7%	Score 192.2	DB 12	Length 1044
Best Local Similarity	73.6%	Pred. No. 1.3e-45		
Matches 245	Conservative	0	Mismatches 88	Indels 0
				Gaps 0

RESULT	14
AAF92354	
ID	AAF92354 standard; cDNA; 464 BP.

DT	15-MAY-2001	(first entry)
XX		
DE	Bovine mammary tissue derived cDNA #67.	
XX		
KW	Bovine; mammary gland; cancer; tumour; angiogenesis; ss	
XX		
OS	Bos taurus.	
XX		
PN	WO200114553-A1.	
XX		
PD	01-MAR-2001.	
XX		
PF	23-AUG-2000; 2000WO-NZ00166.	
XX		
PR	23-AUG-1999; 99US-0150330.	
XX		
PA	(GENE-) GENESIS RES & DEV CORP LTD.	
XX	(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.	
XX		
FI	Havukkala IJ, Glenn M, Griigor MR, Molenaar AJ;	
XX		
DR	WPI; 2001-226619/23.	
XX		

PS Claim 1; Page 59; 97pp; English

CC The present invention relates to proteins derived from bovine
CC mammary gland cells. The invention is useful for stimulating
CC bovine mammary gland cell growth and function, inhibiting the
CC growth of various mammary gland cancer cells, inhibiting
CC angiogenesis and vascularization of tumours, or modulating
CC the growth of blood vessels in a mammal.

Sequence 464 BP; 99 A; 161 C; 120 G; 84 T; 0 other,

Query Match	57.1%	Score	190.2	DB	22	Length	466
Best Local Similarity	80.7%	Pred	No. 3.9e-45				
Matches	222	Conservative	0	Mismatches	53	Indels	0
						Gaps	0
OY	58	atcacctgctctggaagcagcagcaacatctggagtgatctatgtctgtgctgtgtaccaa	117				
Db	1	atcacctgctctcgggaacacagcagaatgtttgagatctgacgtatgttggtgtcccaa	60				
OY	118	caggtgcccaaggtctcagccccacagacctccctcatcagctgctacaaacga	177				
Db	61	cagatcccaagatcgcggccccacagaacagtcacatctttgtgtgactacagaccctctgg	120				
OY	178	atccccaagacgaattctccgcgtccacagctctgggaacacagccaacctgtgacatcaagctcg	237				
Db	121	gtctccgaagcgaattctccgcgtccacagctctgggaacacagccaacctacatcaagctcg	180				
OY	238	ctcccaaggtcgaagacgaagccgattatctctgtcactgtatcaaaagtacttaacatggt	297				
Db	181	ctcccaagcccggaagacgaagcgatattctctgtctatcccccagaccacctaacaatglt	240				
OY	298	gtttctcgacgcgggaacagagctacacgctcctgg	332				
Db	241	gtttctcgacgcgggaacacacctgtgacgtcccgag	275				

RESULT	15
AAH42401	
ID	AAH42401 standard; DNA; 333 BP

AC AAH42401;

DT 01-OCT-2001 (first entry)

DE Nucleotide sequence of variable light chain fragment of clone G93.

KW Antibody, light chain; VL, amyloid protein; blood brain barrier; endothelial cell; brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease; Alzheimer's disease; prion disease; AIDS-related dementia; epilepsy; brain injury; ss.

OS Homo sapiens.

PN WO200144300-A2.

PD 21-JUN-2001

PF 27-NOV-2000; 2000WO-GB04501.

PR 13-DEC-1999; 99US-0170599.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY

PI Webster C, Osbourn J, Ward G, Miller K;

DR WPI; 2001-398131/42.

DR P-PSDB; AAG62957

XX Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Disclosure; Page 103; 109pp; English.
XX

Sequence	333 BP;	71 A;	99 C;	87 G;	76 T;	0 other;	
Query Match	56.9%;	Score	189.6;	DB	22;	Length	333;
Best Local Similarity	73.2%;	Pred.	No.	5.2e-45;			
Matches	243;	Conservative	0;	Mismatches	89;	Indels	0;
						Gaps	0

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Search completed: August 11, 2002, 22:10:21
Job time: 7701 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 22:03:49 ; Search time 1984.69 Seconds
(without alignments)
3511.146 Million cell updates/sec

Title: US-09-786-015-3
Perfect score: 333
Sequence: 1 cagagatgtctgactacagcc.....ccaggtgcacgcgtctgggt 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_to:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	272.2	81.7	333	4	AF172689	AF172689 Ovis arlie
2	269.4	80.9	393	4	BTU32261	U32261 Bos taurus
3	269	80.8	333	4	AF172684	AF172684 Ovis arlie
4	267.4	80.3	333	4	AF172691	AF172691 Ovis arlie
5	267.4	80.3	333	4	AF172693	AF172693 Ovis arlie
6	265.8	79.8	333	4	AF172690	AF172690 Ovis arlie
7	261.4	78.5	393	4	BTU31106	U31106 Bos taurus
8	261	78.4	333	4	AF172697	AF172697 Ovis arlie
9	259.8	78.0	393	4	BTU32249	U32249 Bos taurus
10	259.8	78.0	393	4	BTU32254	U32254 Bos taurus
11	259.6	78.0	330	4	AF015797	AF015797 Bos taurus
12	259.4	77.9	333	4	AF172695	AF172695 Ovis arlie
13	257.8	77.4	330	4	AF172687	AF172687 Ovis arlie
14	257.6	77.4	336	4	AF172688	AF172688 Ovis arlie
15	256.2	76.9	330	4	AF172696	AF172696 Ovis arlie
16	254.8	76.5	538	4	AF040919	AF040919 Ovis arlie
17	254.4	76.4	336	4	AF172698	AF172698 Ovis arlie
18	253.2	76.0	330	4	AF015796	AF015796 Bos taurus
19	253	76.0	330	4	AF172682	AF172682 Ovis arlie
20	253	76.0	333	4	AF015795	AF015795 Bos taurus
21	251.4	75.5	333	4	AF015795	AF015795 Bos taurus
22	251.4	75.5	333	4	AF015801	AF015801 Bos taurus
23	249.8	75.0	333	4	AF015798	AF015798 Bos taurus
24	248.6	74.7	399	4	BTU32250	U32250 Bos taurus
25	248.2	74.5	330	4	AF172692	AF172692 Ovis arlie
26	248.2	74.5	333	4	AF015799	AF015799 Bos taurus
27	248.2	74.5	333	4	AF172701	AF172701 Ovis arlie
28	246.6	74.1	333	4	AF015791	AF015791 Bos taurus
29	246.6	74.1	333	4	AF015792	AF015792 Bos taurus
30	246.6	74.1	333	4	AF015793	AF015793 Bos taurus
31	246.6	74.1	333	4	AF172683	AF172683 Ovis arlie
32	245.2	73.6	336	4	AF023841	AF023841 Bos taurus
33	245.2	73.6	632	4	AF040920	AF040920 Ovis arlie
34	245	73.6	339	4	AF172685	AF172685 Ovis arlie
35	243.4	73.1	333	4	AF015800	AF015800 Bos taurus
36	243.4	73.1	333	4	BTU012799	U012799 Bos taurus
37	242.6	72.9	393	4	BTU32255	U32255 Bos taurus
38	242.2	72.7	368	4	BTU32264	U32264 Bos taurus
39	242	72.7	629	4	AF040916	AF040916 Ovis arlie
40	241.8	72.6	333	4	BTU012801	U012801 Bos taurus
41	241.8	72.6	339	4	AF172694	AF172694 Ovis arlie
42	241.6	72.6	336	4	AF172699	AF172699 Ovis arlie
43	240.4	72.2	629	4	AF040909	AF040909 Ovis arlie
44	240	72.1	336	4	BTU012802	U012802 Bos taurus
45	238.6	71.7	330	4	AF023843	AF023843 Bos taurus

ALIGNMENTS

RESULT	1	333 bp	mRNA	linear	MAM 29-AUG-1999
AF172689	AF172689				
LOCUS	Ovis aries clone 34 immunoglobulin light chain variable region (IGLV) mRNA, partial cds.				
DEFINITION					
ACCESSION	AF172689.1	GI:5602425			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	sheep.				
	Ovis aries				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
	Bovidae; Caprinae; Ovis.				
REFERENCE	1 (bases 1 to 333)				
AUTHORS	White,G.P., Meusen,E.N.T. and Newton,S.E.				
TITLE	A single-chain variable region immunoglobulin library from the				
	abomasal lymph node of sheep infected with the gastrointestinal				
	nematode parasite Haemonchus contortus				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 333)				
AUTHORS	White,G.P., Meusen,E.N.T. and Newton,S.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-JUL-1999) School of Veterinary Science, The Centre				

Db 67 CAGGCTGTGCTACTACGCCGTCTCCGTGTCGGGTCCTCGGCGCAGAGGGTCTCCATC 126
Oy 61 accctctctggaagcagcagacattggaagtaatgctatggtgctggtacacaacg 120
Db 127 ACCTGCTCTGGAGACGACGACACTGTGGACATTAATGTAAGCTGGTTCACACG 186
Oy 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcgagccctcgagatc 180
Db 187 ATCCAGAGATGGCGCCCGCCAGAACCTCATCTATGTGGCAGCAGTCGAGCCTCGGGGTC 246
Oy 181 ccgacagcattctccggtctcaggtctcggaacacagccaccctgacatcagctcgctc 240
Db 247 CCCGACCATTTCTCCGGTCCAGGTCGTGGACACAGCCACCTGACCATCAGCTCGCTC 306
Oy 241 caggtctggaagcagcagcagattatctgctgctatcgaagtaactacagtggtgt 300
Db 307 CAGGCTGAGAGAGAGAGCAGATTAATTTCTGTGCATCTTATCAGATGATACACACCTGTG 366
Oy 301 ttccgacagcggagaccagagctgacgctc 327
Db 367 TTCCGACGCGGAGACCACTGACCGTTC 393

RESULT 3
AF172684 333 bp mRNA linear MAM 29-AUG-1999
LOCUS AF172684
DEFINITION Ovis aries clone 17 immunoglobulin light chain variable region
(IGLV) mRNA, partial cds.
ACCESSION AF172684
VERSION AF172684.1 GI:5802415
KEYWORDS
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.

REFERENCE 1 (bases 1 to 333)
AUTHORS White, G.P., Meusen, E.N.T. and Newton, S.E.
TITLE A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 333)
AUTHORS White, G.P., Meusen, E.N.T. and Newton, S.E.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
FEATURES
source
1. .333
Location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="17"
/tissue_type="abomasal lymph node"
1. .333
/gene="IGLV"
/gene="IGLV"
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/gene="IGLV"
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAD51674.1"
/db_xref="GI:5802416"
/translation="QAVLTQPSVSRSLGQSVSTICGSSNGVNGVNVYQVPGS
APKLIVGATNRASGVDPDRFSGSRFGNTAATLTISLQADEADYICAFYDSNNGVFG
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BASE COUNT 66 a 93 c 92 g 80 t
ORIGIN

Query Match 80.8%; Score 269; DB 4; Length 333;
Best Local Similarity 88.0%; Pred. No. 1.5e-62;
Matches 293; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Oy 1 caggaatgctactcagccgctccctcgtgtcgtggtccctcgagcagaggtctccatc 60
Db 1 CAGGCTGTGCTACTACGCCGTCTCCGTGTCGGGTCCTCGGCGCAGAGGGTCTCCATC 60
Oy 61 accctctctggaagcagcagacattggaagtaatgctatggtgctggtacacaacg 120
Db 61 ACTGCTTTGGAAGACGACGACAACTGTGGATATGTAATATGAGCTGTGTCACAAACG 120
Oy 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcgagcctcgagatc 180
Db 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcgagcctcgagatc 180
Oy 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcgagcctcgagatc 180
Db 181 ccgacagcattctccggtctcaggtctcggaacacagccaccctgacatcagctcgctc 240
Oy 181 CCCGACCATTTCTCCGGTCCAGGTCGTGGACACAGCCACCTGACCATCAGCTCGCTC 240
Db 181 caggtctggaagcagcagcagattatctgctgctatcgaagtaactacagtggtgt 300
Oy 241 caggtctggaagcagcagcagattatctgctgctatcgaagtaactacagtggtgt 300
Db 241 CAGGCTGAGAGAGAGAGCAGATTAATTTCTGTGCATCTTATCAGATGATACACACCTGTG 300
Oy 301 ttccgacagcggagaccagagctgacgctc 333
Db 301 TTCCGACGCGGAGACCACTGACCGTTC 333

RESULT 4
AF172691 333 bp mRNA linear MAM 29-AUG-1999
LOCUS AF172691
DEFINITION Ovis aries clone 81 immunoglobulin light chain variable region
(IGLV) mRNA, partial cds.
ACCESSION AF172691
VERSION AF172691.1 GI:5802429
KEYWORDS
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.

REFERENCE 1 (bases 1 to 333)
AUTHORS White, G.P., Meusen, E.N.T. and Newton, S.E.
TITLE A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 333)
AUTHORS White, G.P., Meusen, E.N.T. and Newton, S.E.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
FEATURES
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1. .333
Location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="81"
/tissue_type="abomasal lymph node"
1. .333
/gene="IGLV"
/gene="IGLV"
/gene="IGLV"
/gene="IGLV"
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAD51681.1"
/db_xref="GI:5802430"
/translation="QAVLTQPSVSRSLGQSVSTICGSSSDVYIGNTVGNFQVPGS
APKLIVGATNRASGVDPDRFSGSSSGNTATLTISLQADEADYICASYDPSDBVFG
SGTRLIVLG"
BASE COUNT 63 a 102 c 90 g 78 t
ORIGIN

Query Match 80.3%; Score 267.4; DB 4; Length 333;
Best Local Similarity 87.7%; Pred. No. 4e-62;

Query Match	Similarity	80.3%	Score 267.4	DB 4	Length 333
Best Local	Similarity	87.7%	Pred. No. 4e-62		
Matches	Conservative	0	Mismatches 41	Indels	Gaps
0Y	1	caggatgtgcgtacccagccgtccctccgtatctgggtccctctggccagaggtctccatc	60		
Db	1	CAGGCTGTGCTACTACAGCCGTCCTCCGTGTCGAAGTCCCTTGGCCACAGGGTCTTCATC	60		
0Y	61	aactgtctctggaagcagcagcaacalttgaggtlaatgtcttatgttggtctgtgtaccacag	120		
Db	61	ACCTGCTCTGGAAAGCAGGACAAAGTGTGGATGTGTAATTAATGTGGGCTGTATCCAAACAG	120		
0Y	121	gtccagagatcagcccccagactccctcatcagtgcttcaacacagcatcgacctgggagtc	180		
Db	121	GTCCAGAGATCAGCCCCAAACTCCTCATTTTATGTGTGCMAACCGCTGTGAGCCCTCGGGGGGTC	180		
0Y	181	cccgaccgattctccggtccaggtctctggaaacacagccacccttgcatacctatgcctgc	240		
Db	181	CCCGACCGATTCTCCGGCTCCAGGTCTGGCAACACAGGCACCTTACACATCAGCTCGCTC	240		
0Y	241	caggtctggagcagagcccatattactctgtgatctgtatccaagtaacttaagatgtgtgt	300		
Db	241	CAGGCTGGAGACAGAGCCGATATTACTGTGTGATTTTATGACCAACGGTATGTTGGGGGT	300		
0Y	301	tctgcagcggagaccaggtctgacctcttggtt	333		

```

RESULT      6
AF172690
LOCUS
DEFINITION  AF172690      333 bp      mRNA      linear      MAM 29-AUG-1999
Ovis aries clone 100 immunoglobulin light chain variable region
(IGLV) mRNA, partial cds.
ACCESSION  AF172690
VERSION
KEYWORDS
SOURCE
ORGANISM   sheep.
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 333)
White, G.P., Meusen, E.N.T. and Newton, S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
Unpublished
2 (bases 1 to 333)
White, G.P., Meusen, E.N.T. and Newton, S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
location/Qualifiers
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/db_xref="taxon:9940"
/clone="100"
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FEATURES
source
gene
CDS

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/note="from the V11 family group; similar to product
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ORGANISM Ovis aries

REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS		Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
TITLE		Bovidae; Caprine; Ovis.
JOURNAL		1 (bases 1 to 333)
REFERENCE		White,G.P., Meusen,E.N.T. and Newton,S.E.
AUTHORS		A single-chain variable region immunoglobulin library from the
TITLE		abomasal lymph node of sheep infected with the gastrointestinal
JOURNAL		nematode parasite Haemonchus contortus
FEATURES		Unpublished
SOURCE		2 (bases 1 to 333)
		White,G.P., Meusen,E.N.T. and Newton,S.E.
		Direct Submission
		Submitted (26-JUL-1999) School of Veterinary Science, The Centre
		for Animal Biotechnology, The University of Melbourne, Parkville,
		Melbourne, Victoria 3052, Australia
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QY	61	acctgccttggaagaagacgaacaacttggaaagtaattgcttatgtggctgtaccacaag 120
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QY	121	gtcccagatcacccccagacctctcatcaagtgtgtacaaccgatcgcgcgcgcgc 180
Db	121	GTCACGAGATCACCCCCAAACTCCTATTATGTGTGCACACGTCGAGCCTCGGGGGT 180
QY	181	ccgcacgatctcccgctccaaggtctcggaaacacagccaccctgacatcaagctgcgc 240
Db	181	CCCACCATTTTCCGCTCCAGGTTTGGAACAACAGGAGCTTTATTATCAATTCCGCTC 240
QY	241	caggcttgaggagccgaagccgattattactgtgtcatcgtgtlcaaagaactaacgttgtt 300
Db	241	CAGGCTTAGAGAGAGAGCCGATTATTACTGTGTGATGTTGTGACAGTAAGCCGACTATT 300
QY	301	ttcggcaacggagaccagagctgaccgtctccttggt 333
Db	301	TTTCGCAGTGGGACCAGGCTGACCGTCTCGGTT 333
RESULT	9	
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DEFINITION	Bos taurus clone 2 immunoglobulin lambda light chain variable	
REGION	(Ylamhdala) rRNA, partial cds.	
VERSION	U32249	
KEYWORDS	U32249.1 GI:1276598	

SOURCE	ORGANISM
REFERENCE	cow.
REFERENCE	Bos taurus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE	1 (bases 1 to 393)
REFERENCE	Ivanov,V.N., Karginov,V.A., Morozov,I.V. and Gorodetsky,S.I.
REFERENCE	Molecular cloning of a bovine immunoglobulin lambda chain cDNA
REFERENCE	Gene 67 (1), 41-48 (1988)
REFERENCE	88329743
REFERENCE	2 (bases 1 to 393)
REFERENCE	Jackson,T., Morris,B.A. and Sanders,P.G.
REFERENCE	Nucleotide sequences and expression of cDNAs for a bovine anti-testosterone monoclonal IgG1 antibody
REFERENCE	Mol. Immunol. 29 (5), 667-676 (1992)
REFERENCE	92261635
REFERENCE	3 (bases 1 to 393)
REFERENCE	Sinclair,M.C., Gilchrist,J. and Aitken,R.
REFERENCE	Molecular characterization of bovine V lambda regions
REFERENCE	J. Immunol. 155 (6), 3068-3078 (1995)
REFERENCE	95403981
REFERENCE	4 (bases 1 to 393)
REFERENCE	Aitken,R.
REFERENCE	Direct Submission
REFERENCE	Submitted (25-JUL-1995) Robert Aitken, Microbiology, Institute of Biomedical and Life Sciences, University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
REFERENCE	location/Qualifiers
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BASE COUNT 79 a 130 c 99 g 85 t
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Matches 285; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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QY 61 acctgctctggaagcagcagcaacattgaggtaatgtcttatgtgtgctgtgaccag 120
DB 127 ACCTGCTCTGGAAGCAGCGCAACGTTGGACGTGGCAATTATGTAGCTGTCCAAACAG 186

QY 121 gtcccgagatcagccccagactcctcctcagtgctgtacacagatcgagcctcgaggatc 180
DB 187 ATCCAGAGATCAGCCCCCAAAACCTCATCTATGATGCGACCACTGGAACCTCGGGGCTC 246

QY 181 ccgcagcagatctccggtctccaggtctcgtggaacacagccaccctgaccatcagctgcgc 240
DB 247 CCCGACCATCTCTCCGGCTCCAGGCTGTGGAACTCAGCCACCTGATGATCAGCTCGCTC 306

QY 241 caggctgagagcagagccgattactactgtgcatcgatcagatcaagaactacagtggtgt 300
DB 307 CAGGCTGAGAGCAGAGCGGATTAATTTCTGTGATCTTATCAAACTGTAAACACAGCTATT 366

QY 301 ttccgagcagggagcagcaggtgacgcgtc 327
DB 367 TTCGGCAGCGGACCACTGACCGCTC 393

RESULT 10
BTU32254 393 bp mRNA linear MM 25-APR-1996
LOCUS
DEFINITION Bos taurus clone 8 Immunoglobulin lambda light chain variable region (Vlambdala) mRNA, partial cds.
ACCESSION U32254
VERSION U32254.1 GI:1276608
KEYWORDS
SOURCE
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae; Bovinae; Bos.
1 (bases 1 to 393)
Ivanov,V.N., Karajinov,V.A., Morozov,I.V. and Gorodetsky,S.I.
Molecular cloning of a bovine Immunoglobulin lambda chain cDNA
Gene 67 (1), 41-48 (1988)
88329743
2 (bases 1 to 393)
Jackson,T., Morris,B.A. and Sanders,P.G.
Nucleotide sequences and expression of cDNAs for a bovine anti-testosterone monoclonal IgG1 antibody
Mol. Immunol. 29 (5), 667-676 (1992)
92261635
3 (bases 1 to 393)
Sinclair,M.C., Gilchrist,J. and Aitken,R.
Molecular characterization of bovine V lambda regions
J. Immunol. 155 (6), 3068-3078 (1995)
95403981
4 (bases 1 to 393)
Aitken,R.
Direct Submission
Submitted (25-JUL-1995) Robert Aitken, Microbiology, Institute of Biomedical and Life Sciences, University of Glasgow, Joseph Black Building, Glasgow G12 800, UK
Location/Qualifiers
1..393
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/organism="Bos taurus"
/db_xref="taxon:9913"
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367..393
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Best Local Similarity 87.2%; Pred. No. 4.6e-60;
Matches 285; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 caggatgtgctgactcagccgctcctcgtgctggttcccttgccgcaagggtcctcacc 60
DB 67 CAGGCTGTGCTGACTACAGCCGCTCCTCCGCTCCGGTACTCGGCCAGAGGCTCCATC 126

QY 61 acctgctctggaagcagcagcaacattgaggtaatgtcttatgtgtgctgtgaccag 120
DB 127 ACCTGCTCTGGAAGCAGCGCAACGTTGGACGTGGCAATTATGTAGCTGTCCAAACAG 186

QY 121 gtcccgagatcagccccagactcctcctcagtgctgtacacagatcgagcctcgaggatc 180
DB 187 ATCCAGAGATCAGCCCCCAAAACCTCATCTATGATGCGACCACTGGAACCTCGGGGCTC 246

QY 181 ccgcagcagatctccggtctccaggtctcgtggaacacagccaccctgaccatcagctgcgc 240
DB 247 CCCGACCATCTCTCCGGCTCCAGGCTGTGGAACTCAGCCACCTGATGATCAGCTCGCTC 306

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Db 367 TTCGGCAGCGGACGACACTGATCGTC 393

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DEFINITION cds.
ACCESSION AF015797
VERSION AF015797.1 GI:2323383
KEYWORDS
SOURCE .
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 330)
AUTHORS Saini,S.S., Jacobs,R. and Kaushik,A.
TITLE Structural features of immunoglobulin variable-region lambda light
chain of BLV-infected cattle
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 330)
AUTHORS Saini,S.S., Jacobs,R. and Kaushik,A.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph,
ON N1G 2W1, Canada

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QY 301 ttccgagcagcgagcagcagcagctgacgtcctc 330
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Db 301 TTCGGCAGCGGACGACACTGACCTGCTCG 330

RESULT 12
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LOCUS Ovis aries clone 96 immunoglobulin light chain variable region
DEFINITION (IGLV) mRNA, partial cds.
ACCESSION AF172695
VERSION AF172695.1 GI:5802437
KEYWORDS
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 333)
AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 333)
AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia

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BASE COUNT 61 a 104 c 95 g 73 t
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Query Match 77.9%; Score 259.4; DB 4; Length 333;
Best Local Similarity 86.2%; Pred. No. 6e-60;
Matches 287; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Db 181 CCCGACCGATTCTCCGGCTCTCAAGTCTGGCAGCAGCAGCACTTAACATCACTGCTC 240
QY 241 cagagctgagagcagcagcagatatactctgtgcatcgatataaagtaactcagtggtc 300
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 19:45:49 ; Search time 2546.98 Seconds
(without alignments)
1923.609 Million cell updates/sec

Title: US-09-786-015-1

Perfect score: 363
Sequence: 1 caggtcagctgcagcagcagtc.....tccctactcaccgtctcctca 363

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_estlhum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	246	67.8	509	10	BE480721 165931 BA
3	244.6	67.4	509	10	BE487664 176725 BA
4	242	66.7	555	9	AV667743
5	241.4	66.5	504	10	BE487301 175972 BA
6	239.6	66.0	505	10	BE589545 195790 BA
7	236.2	65.1	456	10	BE481532 167023 BA
8	235.4	64.8	492	10	BE692159 341738 BA
9	235.4	64.8	583	10	BE846118 232255 BA
10	233.4	64.3	496	10	BE485461 172501 BA
11	233.4	64.3	517	10	BE482028 167666 BA
12	233	64.2	517	10	BE476121 158709 BA
13	232.2	64.0	476	10	BE482206 167909 BA
14	231.8	63.9	488	10	BE589492 195687 BA
15	231.6	63.8	511	10	BE478595 162919 BA
16	230.8	63.6	513	10	BE692944 342818 BA
17	230.4	63.5	412	10	BE482746 168642 BA

18	230.4	63.5	507	10	BE845785
19	230.2	63.4	500	10	BE689490 337581 BA
20	229.4	63.2	441	10	BE485653
21	229.2	63.1	514	10	BE480296
22	229	63.1	413	10	BE481411
23	228.2	62.9	547	10	BE692467
24	228	62.8	396	10	BE230754
25	227.4	62.6	502	10	BE485914
26	227	62.5	598	10	BE588390
27	226.8	62.5	397	10	BE487323
28	226.6	62.4	472	10	BE482203
29	226.6	62.4	502	10	BE485907
30	225.4	62.1	462	10	BE692835
31	225.2	62.0	516	10	BE690115
32	224.2	61.8	409	10	BE482642
33	224.2	61.8	549	10	BE845758
34	224.2	61.8	578	10	BE590022
35	224.2	61.8	581	10	BE588530
36	223.8	61.7	474	10	BE692805
37	223.8	61.7	503	10	BE485219
38	223.6	61.6	390	10	BE482316
39	223.6	61.6	498	10	BE484853
40	223.6	61.6	512	10	BE482341
41	223.4	61.5	456	10	BE480384
42	223.4	61.5	497	10	BE486006
43	222.8	61.4	410	10	BE589795
44	222.8	61.4	498	10	BE480083
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ALIGNMENTS

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LOCUS BE476735 489 bp mRNA linear EST 28-AUG-2000
DEFINITION 160120 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE476735
VERSION BE476735.1 GI:9596268
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 489)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
V0.980904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACGCTATGACAT
BACKWARD: GTTTCACGACGACG
Plate: 28 row: J column: 21
Seq primer: ATTAGTCACACTATAG.
Location/Qualifiers
1..489
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMW SPORT6; site_1: XbaI; site_2: XhoI;

FEATURES

source

TITLE
JOURNAL
COMMENT

Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross-match with the -minscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGAGC
Plate: 123 row: J column: 18
Seq primer: ATTTAGTGACACTATAC.

FEATURES
source
1..504
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI; library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT
ORIGIN
109 a 163 c 128 g 104 t

Query Match
Best Local Similarity 66.5%; Score 241.4; DB 10; Length 504;
Matches 287; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 caggtgcaagctcgaagagtcgggagccagcctggtgaagccctcacagaccctctccctc 60
|||||
DB 80 CAGGTGCACACTGCGGAGTCGGGCCACCGCTGTGTAAGCCCTCACAGACCTCTCCCTC 139
61 acctgacagctctctgattctcaatcaacaaagtatggtggttggttcgacagagct 120
|||||
DB 140 ACCTGCACACATCTCTGGATTCTCATTTGACCACTATGCTGTATCTGGGTCGCCAGGCT 199
QY 121 ccaggaagaagcgcttgagtgagctaggtggtggtccagtggtgacctaaagcctaatac 180
|||||
DB 200 CCAGGGAAGGCGCTGGAGTGGCTGTGTAGTATGACAGTATGGAACACAGACTATGCTC 259
QY 181 acagccctacagtcgccgaactcagcgttcacaaaggagacacctccaagaagccaattctccctg 240
|||||
DB 260 CCAGCCCTGAATAATCCGGCTCAGACATACCAAGGACAACTCCAAAGGCCACTCTCTG 319
QY 241 tcaactgagcagcgttgactactgagagacagcgccattactactgctgcgaatctgtcaat 300
|||||
DB 320 TCAGTAGAGCAGCGCTGACCTGAGAGACGGCCACATATCTACTGTCGAAGCAATATTAAT 379
QY 301 ggtgacagtgcttccctatggttggtgactagtgagccagagactcctactacagctctcc 360
|||||
DB 380 CGTTATCCCTTCTTGATATGATAGATGCTGCTGGGGCCAGGAGACTCCAGGTCACTGCTCACC 439
QY 361 tca 363
|||||
DB 440 TCA 442

RESULT 6
BE589545
LOCUS BE589545
DEFINITION 195790 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE589545
VERSION BE589545.1 GI:9842584
KEYWORDS EST.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

cow.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 505)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross-match with the -minscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGAGC
Plate: 122 row: F column: 3
Seq primer: ATTTAGTGACACTATAC.

FEATURES
source
1..505
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI; library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT
ORIGIN
111 a 149 c 138 g 107 t

Query Match
Best Local Similarity 66.0%; Score 239.6; DB 10; Length 505;
Matches 294; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 1 caggtgcaagctcgaagagtcgggagccagcctggtgaagccctcacagaccctctccctc 60
|||||
DB 80 CAGGTGCACACTGCGGAGTCGGGCCACCGCTGTGTAAGCCCTCACAGACCTCTCCCTC 139
61 acctgacagctctctgattctcaatcaacaaagtatggtggttggttcgacagagct 120
|||||
DB 140 ACCTGCACAGCTCTCTGGATTCTCATTTGACCACTATGCTGTATGTTGACTGGGTCGCCAGGCT 199
QY 121 ccaggaagaagcgcttgagtgagctaggtggtggtccagtggtgacctaaagcctaatac 180
|||||
DB 200 CCAGGGAAGGCGCTGGAGTGGCTGTGTAGTATGAGTGTGTGAAGCAACATATCTTAAC 259
QY 181 acagccctacagtcgccgaactcagcgttcacaaaggagacacctccaagaagccaattctccctg 240
|||||
DB 260 CCAGCCCTGAATAATCCGGCTCAGACATACCAAGGACAACTCCAAAGGCCACTCTCTG 319
QY 241 tcaactgagcagcgttgactactgagagacagcgccattactactgctgcgaatctgtcaat 300
|||||
DB 320 TCAGTAGAGCAGCGCTGACCTGAGAGACGGCCACATATCTACTGTCGAAGCAATATTAAT 379
QY 301 ggtgacagtc---gttccctatggttggtgactagtgagccagagactcctactacagctc 357
|||||
DB 380 GGTGATAGTTGGATACTAATATGATGATGCTGCTGGGGCCAGGAGACTCTGCTCACCCTC 439
QY 358 tccctca 363
|||||
DB 440 TCCTCA 445


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RESULT 7
LOCUS BE481532 456 bp mRNA linear EST 28-AUG-2000
DEFINITION 167023 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE481532
VERSION BE481532.1 GI:9601065
KEYWORDS EST.
SOURCE cown.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 456)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
REFERENCE Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
AUTHORS Wells,K.D.
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
JOURNAL gland cDNA library
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tadslpsi.barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTGAGTCAGCAGC
Plate: 20 row: J column: 7
Seq primer: ATTTAGTGACACTATAG.
FEATURES
source 1. 456
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 101 a 129 c 125 g 101 t
ORIGIN
Query Match 65.1%; Score 236.2; DB 10; Length 456;
Best Local Similarity 83.5%; Pred. No. 1.8e-54;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Db 380 GGTGTAGTATTGATTATAG 400
RESULT 8
LOCUS BG692159 492 bp mRNA linear EST 02-MAY-2001
DEFINITION 341738 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BG692159
VERSION BG692159.1 GI:13933979
KEYWORDS EST.
SOURCE cown.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 492)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
REFERENCE Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
AUTHORS Wells,K.D.
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
JOURNAL gland cDNA library
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tadslpsi.barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTGAGTCAGCAGC
Plate: 41 row: F column: 19
Seq primer: ATTTAGTGACACTATAG.
FEATURES
source 1. 492
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 102 a 152 c 134 g 104 t
ORIGIN
Query Match 64.8%; Score 235.4; DB 10; Length 492;
Best Local Similarity 80.2%; Pred. No. 3.2e-54;
Matches 291; Conservative 0; Mismatches 66; Indels 6; Gaps 1;

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QY      301 ggtgacagtgcttcctatggttggaactagagccaggaactcctactacacgcttc 360
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      385 GGTTAATAATATATATATG-----AGCCTGGGGCCAGAGACTCCTGTGACCGCTCTCC 438
QY      361 tca 363
        |||
Db      439 TCA 441

RESULT  9
BE846118
LOCUS   BE846118 583 bp mRNA linear EST 25-SEP-2000
DEFINITION 232255 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE846118
VERSION BE846118.1 GI:10282942
KEYWORDS EST.
SOURCE EST.
ORGANISM Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovinae; Bos.
REFERENCE 1 (bases 1 to 583)
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
          Wells,K.D.
TITLE      Mapping of Expressed Sequence Tags from a normalized bovine mammary
JOURNAL    gland cDNA library
COMMENT    Unpublished (2000)
CONTACT: Sonstegard TS
          USDA, ARS, Beltsville Agricultural Research Center
          Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
          Tel: 301 504 8416
          Fax: 301 504 8414
          Email: tads@psi.barc.usda.gov
          Single pass sequencing. Bases called and alt-trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -mismatch 12 options.
PCR PRIMERS
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTCACGACGACGACG
Plate: 112 row: P column: 20
Seq primer: ATTTAGTGACACTATAG.
FEATURES
          source
            1..583
              /organism="Bos taurus"
              /db_xref="taxon:9913"
              /clone_lib="BARC 5BOV"
              /tissue_type="pooled"
              /lab_host="DH10B"
              /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
              library made from pooled mRNA isolated from mammary
              tissues at eight physiological, developmental, and disease
              states."
BASE COUNT 117 a 186 c 161 g 119 t
ORIGIN
Query Match 64.8%; Score 235.4; DB 10; Length 583;
Best Local Similarity 80.2%; Pred. No. 3.4e-54;
Matches 291; Conservative 0; Mismatches 66; Indels 6; Gaps 1;

QY      1 caggtcagctgacgagtgaggaccagctgtgaagccctcacagacccttcctc 60
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      79 CAGGTGAGCTGCGGGAGCTAGGCCCGAGCCTGTGAAGCCCTCACAGACCTCTCCCTC 138
QY      61 acctgacagctcctcgtatcattcaacaagatagtggttagtggtgcgcgaagct 120
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      139 ACTGTGACGCTCTCTGATTTCTCATTGACGACTATGCTTATGAGCTGGGTCGCCAGGCT 198
QY      121 ccaggaagagcgctctgagtgactagtggtgtgccagtggtgcaactaagacctataac 180
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      199 CCGGGGAAGGCGCTGAGTGGTGGTGTGTGCACAGTGATGGAACGACAGCTATTAAC 258

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QY      181 acagccctacagtcaccgactcaagcgtcaccaaggagacactccaagaagccaattccctg 240
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      259 CCAGCCCTGAATATCCCGCCCTACCATCACCACCAAGCAACTCCAAAGCCAAAGTCTCTCG 318
QY      241 tcaactgacagcggtgactactgagacacggccattactactggtgcgaatctgcaat 300
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      319 TCAGTGAAGCGCTGACCTGAGACGCGCCACACTACTGTGCAAGGCTATATACT 378
QY      301 ggtgacagtgcttcctatggttggaactagagccaggaactcctactacacgcttc 360
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      379 GGTTAATAATATATATATG-----AGCCTGGGGCCAGAGACTCCTGTGACCGCTCTCC 432
QY      361 tca 363
        |||
Db      433 TCA 435

RESULT  10
BE485461
LOCUS   BE485461 496 bp mRNA linear EST 28-AUG-2000
DEFINITION 172501 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE485461
VERSION BE485461.1 GI:9604994
KEYWORDS EST.
SOURCE EST.
ORGANISM Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovinae; Bos.
REFERENCE 1 (bases 1 to 496)
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
          Wells,K.D.
TITLE      Mapping of Expressed Sequence Tags from a normalized bovine mammary
JOURNAL    gland cDNA library
COMMENT    Unpublished (2000)
CONTACT: Sonstegard TS
          USDA, ARS, Beltsville Agricultural Research Center
          Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
          Tel: 301 504 8416
          Fax: 301 504 8414
          Email: tads@psi.barc.usda.gov
          Single pass sequencing. Bases called and alt-trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -mismatch 12 options.
PCR PRIMERS
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTCACGACGACGACG
Plate: 133 row: J column: 4
Seq primer: ATTTAGTGACACTATAG.
FEATURES
          source
            1..496
              /organism="Bos taurus"
              /db_xref="taxon:9913"
              /clone_lib="BARC 5BOV"
              /tissue_type="pooled"
              /lab_host="DH10B"
              /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
              library made from pooled mRNA isolated from mammary
              tissues at eight physiological, developmental, and disease
              states."
BASE COUNT 108 a 151 c 138 g 99 t
ORIGIN
Query Match 64.3%; Score 233.4; DB 10; Length 496;
Best Local Similarity 79.6%; Pred. No. 1.1e-53;
Matches 289; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY      1 caggtcagctgacgagtgaggaccagctgtgaagccctcacagacccttcctc 60
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      78 CAGGTGAGCTGCGGGAGTGCGGCCCGAGCCTGTGAAGCCCTCACAGACCTGTCCCTC 137
QY      61 acctgacagctcctcgtatcattcaacaagatagtggttagtggtgcgcgaagct 120

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Db	138	ACCTCAGCGTCTCTGGATTCTCATTAAGCCGGGGAAGATGTAGGCTGGGTCGCCAGGCT	197
Qy	121	ccaggaagaagcgctttagtgagctagtggtgtgtccagtggtgtcactaacagcctataac	180
Db	198	CCAGGAAGGGCGCTGGATGGCTCAGTGCATTAAGGCTGGTGGTGAACACAGAGATATAAC	257
Qy	181	acagccctaacagtcctccgaactcaagcgctccacagggagacctccaaagaccaattctccctg	240
Db	258	CCAGCCCTCGAATATCCGAGCTCAGCTTCACCAAGGCAACTCCAAAGGCAAGTCTCTCTTA	317
Qy	241	tcaactgagcaggtgtactactgtagagacagcgccattactactgtgccaatcttcaat	300
Db	318	TCACCTGACACAGGCTACTACTGTGAACACGCGCCACATACTCTGTGGAAGGATTTGAT	377
Qy	301	ggtgacagtgttctcctatgtgttggaaactatgagacacaggaactcctactaacctcc	360
Db	378	GGGTGGATTCGGTAAATGAGACAT---CCCTGTGGGCCACGGAGACTCTGTGTCACCGTCTCC	434
Qy	361	tca	363
Db	435	TCA	437

RESULT	11
BEA82028	
LOCUS	BEA82028 517 bp mRNA linear EST 28-AUG-2000
DEFINITION	167666 BAHC SBOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION	BEA82028
VERSION	BEA82028..1 GI:9601561
KEYWORDS	EST.
SOURCE	COW.
ORGANISM	Bos taurus

REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. 1 (bases 1 to 517)	Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library	unpublished (2000)	Contact: Sonstegard TS
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.			

USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@p1s1.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGAC
Plate: 22 row: E column: 2
Seq primer: AYTtAGGTGACACTATtAG.

FEATURES	SOURCE	Location/Qualifiers
	1.	.517
	/organism="Bos taurus"	
	/db_xref="taxon:9913"	
	/clone_lib="BARC 580V"	
	/tissue_type="pooled"	
	/lab_host="DH10B"	
	/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."	
BASE COUNT	115 a	120 g
ORIGIN	171 c	111 t

Query Match	64.38;	Score 233.4;	DB 10;	Length 517;
Best Local Similarity	77.78;	Pred. No. 1.1e-53;		

	Matches	282:	Conservative	0:	Mismatches	81:	Indels	0:	Gaps	0:
OY	1	caggtgcagctg	cagaagtcggaagtcggaaccagccctg	tgtaagcccttcagaccctctccctc	60					
DB	78	CAGGTGCAGCTCGCGAG	ATTGGGCCCCAACCTCGTGAACCTCTCA	GACCCCTTC	137					
OY	61	acctgcaggtctctcgtatctcattaa	ccaagtatggtgtaagttcgccgaagct	120						
DB	138	ACCTGCACGCATCTGCGAG	TTCATTGACACACTATGCTGTCTCTG	TGGGTCGGCCAAACT	197					
OY	121	ccaagaaagcgcttgatggtgc	taagttggtgctcagtggtgcacataagccataac	180						
DB	198	CCAGGGAATCTCTGGAG	TGGCTTGCTGATATAAACCATTCTGTGGAACCA	CACACACTATAAC	257					
OY	181	acagccctatcagtc	cccgactcagtc	lccacagaaggaacccctc	aagaagccaattctccctg	240				
DB	258	CCAGCCCTTAATCCCGA	ATCCAGATCACCAATCACAGCAAGCAACTCCAA	AAACCAACTCTCTCG	317					
OY	241	tcaatcgagagagtg	tactactatggaacagcgcatctt	actactatgtgsgaaatctgtaat	300					
DB	318	TTTCCTGAGGACCGTGA	CACCTGAGGACACGGCCACATACTACTGTATCA	AAATAATCCCGGGAT	377					
OY	301	ggtagcagtgctctcattg	ttcttgactatggaagcccaagacctctc	ataacgctctcc	360					
DB	378	AAATATGATTCACATAT	GATACATCGAGTCTCTGGGCGCAGGACTTCTGTGTAC	ACCGTCTCC	437					
OY	361	tca	363							
DB	438	TCA	440							

RESULT	12
BEA76121	
LOCUS	BEA76121
DEFINITION	158709 BAC 5BOV Bos taurus cDNA 5' , mRNA sequence.
ACCSSION	BEA76121
VERSION	BEA76121.1
KEYWORDS	G1:9595654
SOURCE	EST.
COW,	
Bos taurus	
ORGANISM	

REFERENCE AUTHORS	TITLE	JOURNAL COMMENT
1 (bases 1 to 518) Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and Wells, K.D.	Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library	unpublished (2000)
Contact: Sonstegard TS USDA, ARS, Beltsville Agricultural Research Center Bldg. 200 Rm 2A, Beltsville, MD 20705, USA		

Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCAAGAG
Plate: 26 row: G column: 1
Seq primer: ATTTAGGTGACACTATTA.
Location/Qualifiers
1..518
FEATURES
source

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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 580V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease

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BASE COUNT 109 a 150 c 149 g 110 t
ORIGIN

Query Match 64.2%; Score 233; DB 10; Length 518;
Best Local Similarity 82.9%; Pred. No. 1.5e-53;
Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 caagtcagctgcagagagtcggagaccagctgtgtgaagccctcaagaccctctccctc 60
DB 97 CAGGTGACGTGCGCGAGTGGGCCCCAGCCTGTGAAGCCCTCAGACGCTCTCCCTC 156
QY 61 acctgcagctctcttgatttcatttaaccaagtatgtgttagttgttcgcgcagact 120
DB 157 ACCTGACGCGTCTGTGATTCTCATTGACAGCATCTGTAAAGCTGATCCGACAGCT 216
QY 121 ccaggaaagcgctgtgagtgtcagtgtgtgtccagtggtgactaacaagcctataac 180
DB 217 CCAGGGAAGCGCTGGAGTCCCTGGGTATACACAGTGTGGAACACAGGCTATTAAC 276
QY 181 acagccctacagtcgccagctcagcgttcacagagagacacccccaagagccaatctccctg 240
DB 277 CCAGCCTGAATCCCGGCTCAGCATATCCAGAGACAATCCAGAGCCAAAGTCTCGCTG 336
QY 241 tcaactgagcagcgtgactactgagagacagcattactactgtgcgaaatctgtcaat 300
DB 337 TCAGTGAAGCGCTGACACTGAGAGACGCGCACATACACTGTGCAAAAAGTTCTTAT 396
QY 301 ggtgacagcttctcctatagt 321
DB 397 GGTGCTGTGCGCATAGTGTGT 417

RESULT 13

BE482206 476 bp mRNA linear EST 28-AUG-2000
LOCUS BE482206
DEFINITION 167909 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE482206
VERSION BE482206.1 GI:9601739
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
AUTHORS 1 (bases 1 to 476)
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
Wells, K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
JOURNAL gland cDNA library
COMMENT Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGACGACGACG
Plate: 22 row: 0 column: 5
Seq primer: ATTTAGTGACACTATAG.
FEATURES
Location/Qualifiers
1..476
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: PCMV SPOT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 98 a 134 c 143 g 101 t
ORIGIN

Query Match 64.0%; Score 232.2; DB 10; Length 476;
Best Local Similarity 80.1%; Pred. No. 2.4e-53;
Matches 305; Conservative 0; Mismatches 58; Indels 18; Gaps 2;

QY 1 caagtcagctgcagagagtcggagaccagctgtgtgaagccctcaagaccctctccctc 60
DB 13 CAGGTGACGTGCGCGAGTGGGCCCCAGCCTGTGAAGCCCTCAGACGCTCTCCCTC 72
QY 61 acctgcagctctcttgatttcatttaaccaagtatgtgttagttgttcgcgcagact 120
DB 73 ACCTGACGCGTCTGTGATTCTCATTGACAGCATATGCTATAGACTGGTCCGCAAGCT 132
QY 121 ccaggaaagcgctgtgagtgtcagtgtgtgtccagtggtgactaacaagcctataac 180
DB 133 CCAGGGAAGCGCTGGAGTCTCTTGGTATTAAGTATGCTGGAACACAGCCTATTAAT 192
QY 181 acagccctacagtcgccagctcagcgttcacagagagacacccccaagagccaatctccctg 240
DB 193 CCAGCCTGAATCCCGGCTCAGCATATCCAGAGACAATCCAGAGCCAAAGTCTCTGT 252
QY 241 tcaactgagcagcgtgactactgagagacagcattactactgtgcgaaatctgtgaaa----- 291
DB 253 TCAGTGAAGCGCTGACACTGAGAGACGCGCACATACACTGTGCAAAAAGTGTGT 312
QY 292 -----tcgtcaatggtgacagctgttcctatagt---tggactactgagccagga 342
DB 313 GGTGTTATGTTGTGTGTACGGTGTGATTATGATTACGTCATGCTGGGCGCAAGGA 372
QY 343 ctccactacacgctctcctca 363
DB 373 CTCCTGTGTCACGCTCTCTCA 393

RESULT 14

BE589492 488 bp mRNA linear EST 28-AUG-2000
LOCUS BE589492
DEFINITION 195687 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE589492
VERSION BE589492.1 GI:9842531
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
AUTHORS 1 (bases 1 to 488)
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
Wells, K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
JOURNAL gland cDNA library
COMMENT Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGACGACGACG
Plate: 122 row: A column: 21
Seq primer: ATTTAGTGACACTATAG.

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XX	RESULT	1
AAA08400	ID	AAA08400 standard; DNA; 363 BP.
XX	AAA08400;	
XX	13-JUL-2000	(first entry)
DE	Carcinoembryonic antigen affinity antibody heavy chain variable region	
KW	Carcinoembryonic antigen; CEA; sheep; monoclonal antibody;	
KW	tumour associated antigen; anti-carcinogenic; cytostatic;	
KW	cancer therapy; ds.	
XX		
OS	Ovls sp.	
XX	WO200012556-A1.	
XX		
PD	09-MAR-2000.	
XX		
PF	20-AUG-1999;	99WO-GH02729.
XX		
PR	28-AUG-1998;	98GB-0018915.
XX		
PA	(KSBI-)	KS BIOMEDIX LTD.
PI	Harrison PJ;	
XX		
DR	WPI: 2000-375618/32.	
XX	P-PSDB: AAY02528.	
PT	A new high-affinity monoclonal antibody that is characterized by an	

PT acid-washed enzyme-linked immunosorbent assay for use in cancer therapy
XX
XX
PS Claim 9; Page 13-14; 21pp; English.
XX
XX
CC The present invention describes a high-affinity monoclonal antibody
CC characterised by an acid-washed enzyme-linked immunosorbent assay (EIA).
CC The antibody is used in cancer therapy. Association of the new antibody
CC with an antigen is favoured over dissociation in vivo and they therefore
CC have longer localisation times at target sites, resulting in a higher
CC concentration of antibodies localised at the target sites. Targeting the
CC antibody to a site in vivo is improved. The concentration of antibody
CC does not need to be too high which reduces side-effects and costs of
CC therapy. The present sequence encodes the heavy chain variable region
CC of a monoclonal antibody having affinity for carcinoembryonic antigen
CC (CEA, a tumour associated antigen), which is used in the exemplification
CC of the present invention.
XX
XX
SQ Sequence 363 BP; 78 A; 110 C; 93 G; 82 T; 0 other;

Query Match 100.0%; Score 363; DB 21; Length 363;
Best Local Similarity 100.0%; Pred. No. 1e-97;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggtgacgtgcagagagtcggagaccagctgtggaagccctacagaccctctccctc 60
Db 1 caggtgacgtgcagagagtcggagaccagctgtggaagccctacagaccctctccctc 60
QY 61 acctgcacgctctctgattctcatcaacaagtatgtttagttggtccgcagagct 120
Db 61 acctgcacgctctctgattctcatcaacaagtatgtttagttggtccgcagagct 120
QY 121 ccagaaagcgcttgagtgtagtggtgtgtgtccagtggtgacataaagcctataac 180
Db 121 ccagaaagcgcttgagtgtagtggtgtgtgtccagtggtgacataaagcctataac 180
QY 181 acagccctaacagtcaccagctcagctacacagagacacccccaagaagcaattctccctg 240
Db 181 acagccctaacagtcaccagctcagctacacagagacacccccaagaagcaattctccctg 240
QY 241 tcaactgcagcgtgactactagagacagcgccattactactgtgcgaatctgtcaat 300
Db 241 tcaactgcagcgtgactactagagacagcgccattactactgtgcgaatctgtcaat 300
QY 301 ggtgacagtgcttcctacttggttggactactgagccagagactcactactcaacgtctcc 360
Db 301 ggtgacagtgcttcctacttggttggactactgagccagagactcactactcaacgtctcc 360
QY 361 tca 363
Db 361 tca 363

RESULT 2
AAT69218
ID AAT69218 standard; DNA; 752 BP.
XX
XX
AC AAT69218;
XX
DT 19-AUG-1997 (first entry)
XX
XX
DE 2E12 sfv DNA.
XX
XX
KW Modified sfv; cell adhesion; artificial ligand; tumour; cancer;
XX
XX
OS gene therapy; retrovirus; vector; 2E12; ss.
XX
XX
OS Not specified.
XX
XX
PN WO9720048-A2.
XX
PD 05-JUN-1997.
XX
PF 27-NOV-1996; 96WO-US19051.

XX
PR 30-NOV-1995; 95US-0007755.
XX
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Fell P, Hayden M, Ledbetter JA, Mittler R, Winberg G;
XX
XX
DR WPI; 1997-310604/28.
XX
XX
PT Modified sfv molecule for mediating adhesion between cells -
PT contains antibody binding site and transmembrane domain of receptor,
PT useful for enhancing immune responses to disease
XX
XX
PS Example 1; Fig 12a; 69pp; English.
XX
XX
CC A nucleic acid sequence (AAT69218) is provided of hybridoma 2E12
CC sfv. It was obtd. as an HindIII/BglII fragment by PCR amplification
CC (see also AAT69223-24). It is used in retrovirus vectors such as
CC pLNC-2e12hlg1B87-ITM (see also AAT69216) and pLNC-2e12hlgCD58GPI
CC (see also AAT69217) that code for novel sfv molecules which have been
CC modified by connecting a transmembrane domain of a cell surface
CC receptor to the antigen binding site of the molecule. This creates
CC artificial ligands that stimulate adhesion between cells and
CC enhance co-stimulatory activity during an immune response against
CC disease. Such vectors can be used for gene therapy of e.g. cancer.
XX
XX
SQ Sequence 752 BP; 188 A; 182 C; 205 G; 177 T; 0 other;

Query Match 57.9%; Score 210; DB 18; Length 752;
Best Local Similarity 73.8%; Pred. No. 2.3e-52;
Matches 267; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 1 caggtgacgtgcagagagtcggagaccagctgtggaagccctacagaccctctccctc 60
Db 385 caggtgacgtgcagagagtcggagaccagctgtggaagccctacagaccctctccctc 444
QY 61 acctgcacgctctctgattctcatcaacaagtatgtttagttggtccgcagagct 120
Db 61 acctgcacgctctctgattctcatcaacaagtatgtttagttggtccgcagagct 120
QY 121 ccagaaagcgcttgagtgtagtggtgtgtgtccagtggtgacataaagcctataac 180
Db 121 ccagaaagcgcttgagtgtagtggtgtgtgtccagtggtgacataaagcctataac 180
QY 181 acagccctaacagtcaccagctcagctacacagagacacccccaagaagcaattctccctg 240
Db 181 acagccctaacagtcaccagctcagctacacagagacacccccaagaagcaattctccctg 240
QY 241 tcaactgcagcgtgactactagagacagcgccattactactgtgcgaatctgtcaat 300
Db 241 tcaactgcagcgtgactactagagacagcgccattactactgtgcgaatctgtcaat 300
QY 301 ggtgacagtgcttcctacttggttggactactgagccagagactcactactcaacgtctcc 360
Db 301 ggtgacagtgcttcctacttggttggactactgagccagagactcactactcaacgtctcc 360
QY 361 tc 362
Db 745 tc 746

RESULT 3
AAT69217
ID AAT69217 standard; DNA; 1510 BP.
XX
XX
AC AAT69217;
XX
XX
DT 19-AUG-1997 (first entry)
XX
XX
DE Retrovirus vector pLNC-2e12hlg1CD58GPI encoding modified sfv.
XX
XX
KW Modified sfv; cell adhesion; artificial ligand; tumour; cancer;

QY		61	acctgcagcgttcctgtagatccattcaacaagaatacgctgtagtgggtcgcgcaggct	12
Dd		80	acctgcacagctctcgtgtttcccatctaactgcatggtgtacactggtgtgccagctc	13
QY		121	cgaagaagcgtgttgagtgcgtaggtggtgtgtccagtgtgtgactaaagaactaac	18
Dd		140	ccgaagaaggtctgtgagtcgtggtgagtgatatgagtaattggaataatgaacacagactaat	19
QY		181	accgcgcctaaagtcgccgactctcgtgtcacccgggacacactccaagaagcaattctccc	24
Dd		200	tccagctctccaatccacgactgtgcatcagcagaagcaactccaagagcgaagtttctcta	25
QY		241	tcactgcgcagcgtgactactagagacacggccattactactgtgcgaatctgtcataat	30
Dd		260	aaaatgacacgctctgnaaactatgatcacacgcccacgctactactctgtgccaaaggatcccc	31
QY		301	ggtgacagtglttcctatggttttgtagctactcgtgagcccggaactctactaccgctctcc	36
Dd		320	tactatagattactatgctatgtagctactcgtggccgaaggaccacgctcacgcgtctcc	37
QY		361	tca tca tca	
Dd		380	tca tca tca	
 RESULT 6 AAT77852 ID AAT77852 standard; cDNA; 420 BP. XX AC AAT77852; DT XX AA77852; DE 03-NOV-1997 (first entry) XX Murrine anti-human class II monoclonal antibody 44H104 HL chain cDNA. XX KX Antibody; heavy chain; variable region; hybridoma cell line 44H104; KW immune response; enhance; stimulate; vaccine; immunodiagnosis; RM antigen delivery; ss. XX OS Mus musculus. XX FH Key Location/Qualifiers FT CDS 1..420 /tag= a FT /note= "Encodes 44H104 heavy chain variable region, FT including secretion signal; termination FT codon not given" XX WO9640941-AI. XX PN 19-DEC-1996. PD PE 07-JUN-1996; 96MO-CA00400. XX PR 07-JUN-1995; 95US-0483576. PA (CONN-) CONNAUGHT LAB LTD. PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH; XX WPI; 1997-077271/07. DR P-PDB; AAM22538. XX PT Recombinant conjugate antibody mol., modified for delivering an PT antigen - elicits enhanced immune response without the use of PT adjuvant to generate antibodies which are useful in vaccines or PS immuno:diagnosis PS PS Example 1; Fig 1B; 64pp; English.				

XX	AAQ11845 standard; DNA; 363 BP.
XX	AAQ11845;
XX	AC
XX	31-JUL-1991 (first entry)
XX	Anti-placental alkaline phosphatase VH gene.
XX	Placental alkaline phosphatase; antibody; cancer; heavy chain;
XX	KLAP; CDR; SS.
XX	Mus musculus.
XX	OS
XX	Key
XX	Location/Qualifiers
XX	91.105
XX	misc_feature
XX	/tag= a
XX	/label= CDRI
XX	148..195
XX	/tag= b
XX	/label= CDR2
XX	292..330
XX	misc_feature
XX	/tag= c
XX	/label= CDR3
XX	EP429242-A.
XX	FN
XX	29-MAY-1991.
XX	PD
XX	14-NOV-1990; 90EP-0312407.
XX	PF
XX	07-SEP-1990; 90GB-0019552.
XX	PR
XX	17-NOV-1989; 89GB-0026045.
XX	PA
XX	(UNITL) UNILEVER PLC.
XX	Verhoeyen ME;
XX	PI
XX	WPI: 1991-157662/22.
XX	DR
XX	P-PSDB; AAR11984.
XX	PT
XX	Synthetic specific binder for human placental alkaline
XX	phosphatase - for treating and diagnosing cancers e.g. breast,
XX	ovarian and colon cancers and pleural effusions
XX	SS
XX	Disclosure; Fig 1; 28pp; English.
XX	XX
XX	The murine anti-PLAP VH gene contains 3 CDRs which are used to reshape
XX	CC the human anti-PLAP VH gene (AAQ11847). The murine anti-PLAP VH gene
XX	CC (AAQ11846) CDRs were used to reshape the human anti-PLAP gene VK
XX	CC (AAQ11848). The specific binder for human PLAP contains at least
XX	CC one of the former 3 CDRs and/or at least one of the latter CDRs.
XX	CC The produced antibodies are more readily tolerated when administered
XX	CC to a human patient. Antibody reagents can be used to identify, e.g.
XX	CC by serum testing or imaging, and/or to treat PLAP-producing cancers.
XX	CC Such cancers can occur as, e.g. breast cancer, ovarian cancer and
XX	CC colon cancer or can manifest themselves as liquids such as pleural
XX	CC effusions.
XX	Sequence 363 BP; 98 A; 94 C; 94 G; 77 T; 0 other;
XX	50

Query Match	53.3%	Score 193.4	DB 12	Length 363
Best Local Similarity	70.8%	Pred. No. 1.5e-47		
Matches 257	Conservative	0	Mismatches 106	Indels 0
				Gaps 0

Qy	Db
1	1
61	61
120	120

QY	121	ccaggaagagcgcttgagtgtagtgcggtgctgcacgaagccttaac	180
Db	121	ccaagaagaaggctccgagtggtgcgtgcgaatacaggaacgaataatcat	180
QY	181	acaagccctacagctcccgactaagcgtaccagaaggacacctccaaagagccaaattctcctg	240
Db	181	tcaagctctacatactcagactgagcatcaacaagataataaccgaagccgaagtctctta	240
QY	241	tcaatctgcagcgtgactactcgtagagacaagccattactactcgttggaattctgcaat	300
Db	241	aaactgaacacgtccgcaaacatgagacacagcccgtaactactcgtgcacaaaccccaactac	300
QY	301	ggtgacagctgtctcccttaagtgtttgactactggagcccaagactcctacacacggtctcc	360
Db	301	ggtgacagcactagcgtggggcgtatgtaactcgtgggtcgaaggaacctcagtcaccggtctcc	360
QY	361	tca 363	
Db	361	tca 363	

RESULT 9

ID AAT40806 standard; cDNA to mRNA; 414 BP.

AC AAT40806;

DT 10-FEB-1997 (first entry)

DE Mab 10.1 heavy chain, directed against type II phospholipase A2.

KM Monoclonal antibody; phospholipase; myocardial infarction;
 KW pancreatitis; cerebral infarction; acute kidney failure; colitis;
 KW chronic rheumatism; adult respiratory distress syndrome;
 KW cardiac shock; treatment; preclinical testing; disease; hybridoma;
 KW ss.

05 Mus musculus.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
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36	36	36
37	37	37
38	38	38
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40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
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49	49	49
50	50	50
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54	54	54
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89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
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96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

```
FT      /*tag= a
FT      /product= Monoclonal antibody heavy chain.
```

PN W09620959-A1.

PD 11-JUL-1996.

PF 27-DEC-1995; 95WO-JP02714.

PR 29-DEC-1994; 94JP-0340006.

PA (YAMA) YAMANOUCHI PHARM CO LTD.

PI Kawauchi Y, Masuho Y, Takasaki J, Yasunaga T;

DR WPI; 1996-333946/33.

XX

PT for treatment of myocardial and cerebral infarction

PS Example 6; Figure 14; 69pp; Japanese.

CC Monoclonal antibodies which inhibit type II phospholipase A2 are

CC Infarction, acute kidney failure, chronic rheumatism, cardiac shock,

CC antibodies were generated by immunising Balb/C mice with recombinant

CC fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas

CC Active clones were isolated including 12H5, 1.4 and 10.1. These

WFL, 1231-4/5550/44.
DN
XX

xx
os
Synthetic.

```

XX FH Key Location/Qualifiers
FT misc-feature 1..714
FT /*tag- a
FT /*tag- "encodes single chain Fv fragment of
FT antibody 366"
FT misc-feature 715..738
FT /*tag- b
FT /*tag- "Linker sequence"
FT /*tag- 739..0
FT /*tag- c
FT /*tag- "encodes streptavidin"
XX PN WO9734634-A1.
XX PD 25-SEP-1997.
XX PF 20-MAR-1997; 97WO-0504427.
XX PR 20-MAR-1996; 96US-0013703.
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PI Cheung NV, Guo H, Larson SM, Rivlin K, Sadelain M;
XX DR WPI; 1997-479996/44.
XX PT Recombinant single chain anti-disialoganglioside GD2 antibody -
XX PT useful to detect tumour cells expressing GD2 and to target
XX PT therapeutic agents, e.g. toxins, to such cells
XX PS Disclosure; Page 13; 31pp; English.
XX CC The present sequence encodes a recombinant single chain peptide,
XX CC 366-scFv-streptavidin. The peptide is an antibody construct comprising
XX CC the variable regions of the heavy and light chains of an antibody against
XX CC disialoganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occurs
XX CC in many tumours types including neuroblastoma, osteosarcomas and other
XX CC soft tissue sarcomas, medulloblastomas, high grade astrocytomas,
XX CC melanomas and small cell lung cancer. The peptide can be detectably
XX CC labelled, preferably with 99m-Tc, for tissue imaging of cells expressing
XX CC GD2. It can also be used to target delivery of a therapeutic or
XX CC pre-therapeutic agent, such as a toxin, streptavidin (e.g. present
XX CC sequence) or a pro-drug converting enzyme, to cells expressing GD2. The
XX CC peptide may further comprise CD8 to facilitate the formation of
XX CC GD2-targeted lymphocytes. T cells containing the peptide can also be used
XX CC to target GD2-producing tumour cells.
XX SQ Sequence 1173 BP; 270 A; 334 C; 340 G; 229 T; 0 other;

Query Match 51.6%; Score 187.4; DB 18; Length 1173;
Best Local Similarity 71.9%; Pred. No. 1.3e-45;
Matches 261; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 1 caggtgagctgcagagctgcggaccagcctggtgaagccctcaagaccctccctc 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 358 caggtgagctgcagagctgcggaccagcctggtgaagccctcaagaccctccctc 417
QY 61 accgcagcgtctcgtgattcattcaacaagatggtttagttggtcgcagagct 120
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 418 actgcacactgtctcgtggtttcattcaacaattatggtgacactggttcgcagagct 477
QY 121 ccaaggaaagcgtctgtagtgcagtggtggtccagtggtgcactcaagaccctaaac 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 478 ccaaggaaagcgtctgtagtgcagtggtggtccagtggtgcactcaagaccctaaac 537
QY 181 acagcctacagtcgcagctcagcgttcacagaggaacacctcacaagaccattccctg 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 538 tcgctcttattgtccacagtcagtcacagaggaacacacacagcagagcttcttcta 597
QY 241 tcaatgagcagcgtgactactgaggaacagcatttactactgtggaatctgtaaat 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

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DB 598 aaaaatgaacagctcgaacatgacacagccatgtactactgtccagtcgggggggt 657
QY 301 ggtgacagctgtctcctactgattggtgactactgagcccaagactcctaccagctcc 360
   || ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 658 aactaagg-----catgcttgcactactggtggtcagaagaccctcagtcacagctcc 711
QY 361 tca 363
   |||
DB 712 tca 714

RESULT 12
AAZ31382
ID AAZ31382 standard; DNA; 351 BP.
XX AC AAZ31382;
XX DT 07-FEB-2000 (first entry)
XX DE MMASWS1H M. musculus A.SW mRNA for ASWS1 antibody heavy chain.
XX KW Monoclonal antibody; Mab; 1A7; GD2; immune response; melanoma;
XX KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
XX KW tumor-associated antigen; ss.
XX OS Mus sp.
XX PN US5977316-A.
XX PD 02-NOV-1999.
XX PF 16-JAN-1996; 96US-0591196.
XX PR 17-JAN-1995; 95US-0372676.
XX PA (KENT ) UNIV KENTUCKY.
XX PI Foon KA, Chatterjee SK, Chatterjee M;
XX DR WPI; 1999-619711/53.
XX PT Monoclonal antibody 1A7 which elicits an anti-GD2 immunological
XX PT response, useful for the development of products for the detection and
XX PT treatment of cancers -
XX PS Disclosure; Fig 13B; 74pp; English.
XX CC The invention provides a monoclonal antibody (Mab) designated 1A7, which
XX CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
XX CC humans. Mab 1A7 has defined light and heavy chain variable region
XX CC sequences. The Mab 1A7 and polypeptides can be used for eliciting an
XX CC anti-GD2 immune response. The polypeptides can also be used for
XX CC detecting or purifying anti-GD2 antibody. The products can be used for
XX CC treating GD2-associated diseases, e.g. melanoma, neuroblastoma, glioma,
XX CC soft tissue carcinoma, and small cell carcinoma. They can be used for
XX CC palliating the disease or for reducing the risk of recurrence. Sequences
XX CC AAZ31373-90 represent sequences that closely matched Mab 1A7 heavy chain
XX CC variable region encoding sequence.
XX SQ Sequence 351 BP; 95 A; 87 C; 88 G; 80 T; 1 other;

Query Match 51.5%; Score 187; DB 20; Length 351;
Best Local Similarity 72.2%; Pred. No. 1.2e-45;
Matches 260; Conservative 0; Mismatches 91; Indels 9; Gaps 1;

QY 1 caggtgagctgcagagctgcggaccagcctggtgaagccctcaagaccctccctc 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 caggtgagctgcagagctgcggaccagcctggtggtggtgcaccccaagaccctgctccatc 60
QY 61 accgcagcgtctcgtgattcattcaacaagatggtttagttggtcgcagagct 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 acatgcacactgtctcgtggtttcattcaagatagtgtaacactggttcgcagagct 120

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Oy 121 ccaggaagcgcttgatggtcagggtggtgtccagtggtgactaacagcctataac 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ccaggaagagggctctgagggctgggaatgatttgggtgtggaacacagactataat 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 181 acagccctacagtcgccagtcagcgtcaccagggacacccccaagaagccaattccctg 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 tcagctccaataaccagagcagtcacgaagaagacaactccaagaagccaagtttctta 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 241 tcactgagcagcgctgactactgagggacagcgccatttactactggtcgaatctgtcaat 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 aaatgaacagtcgtcaaacatgacacagccatgtactactgtgccagagatggttac 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 301 ggtgacagtcgtcctatggttgactactgagccagcagactccttaccacagctctcc 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 tacgac-----tatgctatgactactgtgggtcagaagaccctcagtcacgcctcc 351

RESULT 13
AAT43413
ID AAT43413 standard; cDNA to mRNA; 357 BP.
XX
AC AAT43413;
XX
DT 17-FEB-1997 (first entry)
XX
DE Xenograft antibody IH21H7 heavy chain variable region cDNA.
XX
KM Xenograft rejection; xenotransplantation; organ transplant;
KM animal model; pig; monoclonal antibody; IH21H7; ds.
XX
OS Rattus sp.
XX
Key Location/Qualifiers
FH 1.357
FT /tag= a
FT /product= Immunoglobulin variable region
FT /standard_name= Ig heavy chain variable region
FT /label= VH_Region
FT /note= "IH21H7 heavy chain variable region"
FT misc_RNA
FT 1..291
FT /tag= b
FT /standard_name= Ig heavy chain variable segment
FT /label= VH_Segment
FT /note= "variable segment of IH21H7 heavy chain
FT misc_RNA
FT 292..312
FT /tag= c
FT /standard_name= Ig Heavy chain diversity segment
FT /label= D_Segment
FT /note= "diversity segment of IH21H7 heavy chain
FT misc_RNA
FT 313..357
FT /tag= d
FT /standard_name= Ig heavy chain joining segment
FT /label= JH_Segment
FT /note= "joining segment of IH21H7 heavy chain
FT misc_RNA
FT 1..90
FT /tag= e
FT /standard_name= Framework region 1
FT /label= FR-1
FT /note= "framework region 1 of IH21H7 heavy chain
FT misc_RNA
FT 91..105
FT /tag= f
FT /standard_name= CDR-1
FT /label= CDR-1
FT /note= "complementarity determining region 1 of
FT misc_RNA
FT 106..151
FT /tag= g
FT /standard_name= Framework region 2

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FT /label= FR-2
FT /note= "framework region 2 of IH21H7 heavy chain
FT misc_RNA
FT 152..198
FT /tag= h
FT /standard_name= CDR-2
FT /label= CDR-2
FT /note= "complementarity determining region 2 of
FT misc_RNA
FT 199..291
FT /tag= i
FT /standard_name= Framework region 3
FT /label= FR-3
FT /note= "framework region 3 of IH21H7 heavy chain
FT misc_RNA
FT 292..324
FT /tag= j
FT /standard_name= CDR-3
FT /label= CDR-3
FT /note= "complementarity determining region 3 of
FT misc_RNA
FT 325..357
FT /tag= k
FT /standard_name= Framework region 4
FT /label= FR-4
FT /note= "framework region 4 of IH21H7 heavy chain
FT
XX WO9636358-A1.
XX 21-NOV-1996.
XX
XX 14-MAY-1996; 96MO-US06804.
XX
XX 15-MAY-1995; 95US-0440621.
XX
XX (CEDA-) CEDARS SINAI MEDICAL CENT.
XX Cramer DV, Makowka L, Wu G;
XX WPI; 1997-011852/01.
XX P-PsDB; AAM06204.
XX
XX Inhibiting xenograft rejection by modifying antigen expression of
XX the graft - prevents binding of anti-donor antibody and prolongs
XX graft survival
XX
XX Claim 7; Page 113-114; 135pp; English.
XX
XX A cDNA clone (AAT43413) codes for the variable heavy chain segment
XX (AAM06204) of the LEW rat anti-porcine xenograft monoclonal antibody
XX 1H21H7. It was obt. from a 1H21H7 heavy chain cDNA library by
XX phage display and PCR amplification, and can be used to produce
XX recombinant 1H21H7 antibody fragments, e.g. Fab'2 and Fab'.
XX These block binding of preformed anti-donor xenograft antibodies in
XX a recipient animal serum to antigen expressed by endothelial cells
XX of the xenograft, i.e. they inhibit antibody-mediated rejection,
XX thereby prolonging the survival of the pig xenograft in the
XX recipient.
XX
XX Sequence 357 BP; 89 A; 97 C; 92 G; 79 T; 0 other;
XX
XX
XX Query Match 51.3%; Score 186.4; DB 18; Length 357;
XX Best Local Similarity 71.8%; Pred. No. 1.8e-45;
XX Matches 260; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
Oy 2 aggtcagctgcagagagtcgggacccagcctggtgaagccctacagaccctccctca 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 aggtcagctgcagagagtcgggacccagcctggtgacagccctacagaccctctctca 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 62 cctgacagctctcgtatcattcaacaagatggtctagcttggtcgcagagctc 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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FT /note= "no STOP codon given"

XX MO9636361-A1.

PN 21-NOV-1996.

XX 16-MAY-1996; 96MO-US07113.

XX 18-MAY-1995; 95US-0443540.

XX (UNMI) UNIV MICHIGAN.

XX Glick GD, Swanson PC;

XX WPI: 1997-011854/01.

DR P-PSDB; AAM07437.

XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT develop prods. for diagnosis and treatment of disorders, e.g.
PT glomerulonephritis or systemic lupus erythematosus

XX Example; Fig 9; 102pp; English.

CC The present sequence encodes the heavy chain variable region of the
CC group II/8 putative consensus anti-DNA monoclonal antibody (Mab),
CC which has a high affinity for single stranded DNA, low or no
CC affinity for double stranded DNA and specifically binds a DNA
CC hairpin. The Mab can be used to diagnose disorders associated with the
CC pathological complexation of DNA, e.g. inflammatory
CC glomerulonephritis and systemic lupus erythematosus. It can also be
CC used to generate reagents to screen for pharmaceutical agents, and
CC treat and/or prevent an above disorder.
CC The sequence was derived by aligning homologous anti-DNA Mab cDNA,
CC whose sequences have been published, as well as several Mab of
CC other specificities obtained from a database search.

XX Sequence 369 BP; 93 A; 95 C; 92 G; 89 T; 0 other;

Query Match 51.0%; Score 185; DB 18; Length 369;

Best Local Similarity 72.6%; Pred. No. 4.6e-45;
Matches 268; Conservative 0; Mismatches 95; Indels 6; Gaps 2;

QY 1 caggctgacgtgagagtcgagccagcctgtgtaagccctcacagaccctccctc 60
DB 1 caggctgacgtgagagtcgagccagcctgtgtaagccctcacagaccctccctc 60
QY 61 acctgacggtctctggtatctcatcaaccaagatggtgttagtgcgcagagct 120
DB 61 acctgacggtctctggtatctcatcaaccaagatggtgttagtgcgcagagct 120
QY 121 ccaggaaaggcgttgatggtgagtggtgt--gtccagtggtgacccaagcctat 177
DB 121 ccaggaaaggcgttgatggtgagtggtgt--gtccagtggtgacccaagcctat 180
QY 178 aacacagccctacagtcgccagtcacagcgttcacagagcaccctccaagacattcc 237
DB 181 aatcggtctcatgtccagcagcagcatcagcaagaagacacattccaagagcaatttc 240
QY 238 ctgtcacgtgagcagctgactactgaggaacagcgccattactactgtgcgaattctgc 297
DB 241 ttaaaatgacacagctcgcaaaactgacacagccatgactactgtgcagacatctc 300
QY 298 ---aatggtagcagtggtctctttagtggtagtactgagccagagcctactacc 354
DB 301 ccttaaggtaactaactgactatgactatgactactggtgcaagaacactcagtcacc 360
QY 355 gtctcctca 363
DB 361 gtctcctca 369

Search completed: August 11, 2002, 22:10:19
Job time: 7699 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 19:46:55 ; Search time 1984.69 Seconds
(without alignments)
3827.466 Million cell updates/sec

Title: US-09-786-015-1
Perfect score: 363
Sequence: 1 cagctgcagctgcagagctc.....tccactccagctcccca 363

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	265.4	73.1	456	4	OAVRA17IG	249176 O.aries MRN
2	254.2	70.0	456	4	OAVRA10IG	249175 O.aries MRN
3	251	69.1	426	4	OAVRB11IG	249192 O.aries MRN
4	251	69.1	450	4	OAVRB6IG	249172 O.aries MRN
5	251	69.1	456	4	OAVRB15IG	249159 O.aries MRN
6	251	69.1	458	4	OAVRA4IG	249170 O.aries MRN
7	249.4	68.7	369	4	AF172680	AF172680 Ovis arle
8	249.2	68.7	461	4	OAVRA4IG	249156 O.aries MRN
9	247.6	68.2	366	4	AF172674	AF172674 Ovis arle
10	247	68.0	449	4	OAVR21IG	249166 O.aries MRN
11	246.6	67.9	447	4	OAVRB1IG	249171 O.aries MRN
12	246.2	67.8	458	4	OAVR12IG	249164 O.aries MRN
13	246	67.8	366	4	AF172667	AF172667 Ovis arle
14	246	67.8	366	4	AF172670	AF172670 Ovis arle
15	246	67.8	458	4	OAVR11IG	249158 O.aries MRN
16	244.8	67.4	429	4	OAVRB7IG	249193 O.aries MRN
17	244.6	67.4	422	4	OAVR20IG	249165 O.aries MRN
18	243	66.9	363	4	AF172668	249167 O.aries MRN
19	242.8	66.9	430	4	OAVG10IG	249160 O.aries Imm
20	242.8	66.9	453	4	OAVR3IG	249161 O.aries MRN
21	242.2	66.7	462	4	BTU55202	U55202 Bos taurus
22	241.8	66.6	469	4	OAVR15IG	249169 O.aries MRN
23	240.2	66.2	357	4	AF172666	AF172666 Ovis arle
24	239.8	66.1	360	4	AF172671	AF172671 Ovis arle
25	239.4	66.0	351	4	AF172659	AF172659 Ovis arle
26	238.6	65.7	452	4	OAVRB14IG	249173 O.aries MRN
27	238	65.6	1581	4	BTIG61HCX	X62916 B. taurus MR
28	235.4	64.8	350	4	OAVR10IG	249168 O.aries MRN
29	235	64.7	360	4	AF172665	AF172665 Ovis arle
30	235	64.7	457	4	OAVR18IG	249167 O.aries MRN
31	235	64.7	736	4	OAV7AIG	249186 O.aries Imm
32	235	64.7	847	4	OAV1BIG	249188 O.aries Imm
33	234.2	64.5	406	4	OAI6VRB3	250036 O.aries MRN
34	234	64.5	475	4	OAVR5IG	249178 O.aries MRN
35	233.4	64.3	455	4	OAVRB2IG	249174 O.aries MRN
36	233.4	64.3	739	4	OAVRA19IG	249177 O.aries MRN
37	233.4	64.3	1923	4	OAVSAIG	249187 O.aries Imm
38	233.4	64.3	360	4	AF172664	X59994 O.aries MRN
39	231.8	63.9	430	4	OAVGE70IG	AF172664 Ovis arle
40	231.8	63.9	455	4	OAVR6IG	249181 O.aries Imm
41	231.8	63.9	507	4	TTR320196	249163 O.aries MRN
42	231.8	63.9	507	4	TTR320196	AJ320196 Tursteps
43	231.6	63.8	351	4	AF172660	AF172660 Ovis arle
44	231	63.6	351	4	AF097208	AF097208 Bos tauru
45	231	63.6	408	4	BTU49782	U49782 Bos taurus

ALIGNMENTS

RESULT 1
OAVRA17IG 456 bp MRNA linear MAM 04-FEB-1998
LOCUS O.aries mRNA for immunoglobulin mu heavy chain variable region
(clone VRA17).
ACCESSION Z49176
VERSION Z49176.1 GI:794120
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain; joining region; variable region.
SOURCE Sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 456)
AUTHORS Dufour V.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
REFERENCE 2 (bases 1 to 456)
AUTHORS Dufour V., Malinge S. and Nau F.
TITLE The sheep Ig variable region repertoire consists of a single VH family

JOURNAL	J Immunol.	156 (6),	2163-2170 (1996)
MEDLINE	96310953		
FEATURES			
source	Location/Qualifiers		
gene	1..456		
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	/clone="Vra17"		
	/tissue_type="spleen"		
	/rearranged		
	37..456		
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	37..>456		
	/gene="VH"		
	/codon_start=1		
	/product="VH region precursor"		
	/protein_id="CA89045.1"		
	/db_xref="GI:794121"		
	/translation="MNPIMTLLFVLSAPRGVLSQVRLQESGPSLYKPSQSLTCTVSS GFSLSNANVMDVNRQAPGCKVPTPLMGLSSDSGDTYINPAKSRSTRITRQNSQVLSLS SVTTEDAVYICARTWISGCAGSIDYWGPELLVTS"		
sig_peptide	37..87		
	/gene="VH"		
	88..456		
	/gene="VH"		
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	385..456		
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	/note="D-JH region"		
BASE COUNT	88 a 144 c 127 g 97 t		
ORIGIN			
Query Match	73.1%; Score 265.4; DB 4; Length 456;		
Best Local Similarity	83.2%; Pred. No. 1.1e-69;		
Matches 302: Conservative	0: Mismatches 61; Indels 0; Gaps 0;		
QY	1	caagtcgacgctgcagagatgcggagaccagcctgtgtgaagccctcacagaacctctccctc 60	
DB	94	CAGTGCCTGCTCAGAGATCGGGACCCAGCCCTGTGAAGCCCTTCACAGACCTTCCTCC 153	
QY	61	acctgacagctctcgtgattctcatcaacaagtagtgggtgagtgtggtgcgcagagct 120	
DB	154	ACCTGCACGCTCTTGGAATTCATTAAACCAACATGCTGTGAGCTGGGTCGCCAGGCT 213	
QY	121	ccaaggaagacgcttgatgtgctagtgatgtgtcgtccagctgctgacatacagccataac 180	
DB	214	CCAGGAAGAGTCCCGAGTGGCTGTGTGTGAACAGATGAGTGAAGCAACATACATAAC 273	
QY	181	aaagccctacagctccgagctacagctgcacaggaagcaacctccagaagccaattccctg 240	
DB	274	CCGGCCCTGAAATCCCGGGCAGCATACACAGGAGACGCTCCMAAGGCCAATCTCCCTG 333	
QY	241	tcaactagagagtgtaactactagagacagagccattactactgtgcgaatctgcaat 300	
DB	334	TCACTAGACAGGATGACATGAGGACGGGCGGTGTACTGTGCCGCCACTTGAT 393	
QY	301	ggtcagagtgctcctatggtgttgtaactactgagacccagagactcctaactacagctcc 360	
DB	394	AGTGGCTGTGCTTGTGTGTTCTATCAGACTCTGGGCCCCAGAGACTCTGTGTCACGCTCC 453	
QY	361	tcaa 363	
DB	454	TCA 456	
RESULT 2			
LOCUS	OAVRA10IG	456 bp	mRNA linear MAM 04-FEB-1998
DEFINITION	O.aries mRNA for immunoglobulin mu heavy chain variable region (clone VRA10).		
ACCESSION	Z49175		
VERSION	Z49175.1	GI:794118	
KEYWORDS	diversity1 region; immunoglobulin; immunoglobulin heavy chain;		

SOURCE		Joining region; variable region.
ORGANISM	Ovis aries	Sheep.
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
AUTHORS	Bovidae; Caprine; Ovis.	
JOURNAL	1 (bases 1 to 456)	
TITLE	Dufour V.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA	
TITLE	1172, IBMG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022	
JOURNAL	2 (bases 1 to 456)	
MEDLINE	Dufour,V., Mallinze,S. and Nau,F.	
FEATURES	The sheep Ig variable region repertoire consists of a single VH family	
SOURCE	J. Immunol. 156 (6), 2163-2170 (1996)	
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	/db_xref="taxon:9940"	
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	/gene="VH"	
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	/db_xref="GI:794119"	
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	sig_peptide	37..87
	/gene="VH"	
	V_region	88..456
	/gene="VH"	
	/product="VH region"	
	D_segment	385..456
	/gene="VH"	
	/note="D-JH region"	
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	ORIGIN	
	Query Match	70.0%; Score 254.2; DB 4; Length 456;
	Best Local Similarity	81.3%; Pred. No. 2.7e-66;
	Matches 295; Conservative	0; Mismatches 68; Indels 0; Gaps 0;
Gy	1	caggtgcacgctcgaagatcgaggaccagccgctgtgtgaagccctcaaaccttcctc 60
Db	94	CAGGTGCACGCTCGAAGAAGCGGGACCACGCCCTGTGAAGCCCTCACAGACCCCTCCTC 153
Gy	61	aacctcacgctctcggattccattacaacaaagtatggtgttagttggtccgcaagct 120
Db	154	AACTCGACGCGTTCTCGANTCTCATTAACACACATATTATGTAGCGTCGGGCCAGGCT 213
Gy	121	ccaagaanaagcgcttgatggtgcttaagttggtgtgtcctcagtggtgcaatacagcctataac 180
Db	214	CCAGGAAAAGGCGACTGAGAGTGCGTGTGATGACATATATGCTGGTGAAGTAAGAATAATAGC 273
Gy	181	aaagcctcaagatccccgactacaggtccacacagggagacacctccaagaaccaattctccctg 240
Db	274	CCGGCCCTGTAACCCCCCGCTCAGCTCATCCACAAGGACACCTCCAAAGCCAAGTCTCCCTG 333
Gy	241	tcaactgagcaggttactactatgagaaacagcgccattactactgtgcgaaatcgtcaat 300
Db	334	TCACTGACGAGCGGTACACACTGAGACACAGGCCGCTGTCTACTGTGCAAGAGATCAGCCT 393
Gy	301	ggtgacagtgcttccattatggttgtgactatggaagccaggaactctaactcaacgctccc 360

Db 394 AGTAGGCGCTGTTGGTATACGACTACTGGGCCCCAGAGACTAGTGTACCGTCTCC 453
QY 361 tca 363
Db 454 TCA 456

RESULT 3
LOCUS OAVRB11G 426 bp mRNA linear MAM 04-FEB-1998
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
(clone VRB11).
ACCESSION 249192
VERSION 249192.1 GI:794127
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 426)
AUTHORS Dufour,V.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
REFERENCE 2 (bases 1 to 426)
AUTHORS Dufour,V. and Nau,F.
TITLE Sheep immunoglobulin mu heavy chain variable region sequence
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
1..426
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="VRB11"
/tissue_type="spleen"
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1..426
/gene="VH"
1..>426
/gene="VH"
/codon_start=1
/product="VH region precursor"
/protein_id="CAA89051.1"
/db_xref="GI:794128"
/translation="MNPLWTLFLVLSAPRGVLSQVRLQSGSLVSKSSQTLSTCTVS
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1..51
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52..426
/gene="VH"
/product="VH region"
349..426
/gene="VH"
/note="D-JH region"
BASE COUNT 87 a 128 c 116 g 95 t
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Best Local Similarity 82.1%; Pred. No. 2, 6e-65;
Matches 303; Conservative 0; Mismatches 60; Indels 6; Gaps 1;

QY 1 caggtcagctgcaggaagtcggagccagcctgtgaagccctcaagaccctctccctc 60
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Db 58 CAGGTGCGGCTGCAGAGTCGGAGCCAGCGCTGTGAAGCTTCACAGACCTCTCCCTC 117
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QY 61 acctgcagcgtctctgattctcattcaacaagatagtggttagttgggtccgcaggtc 120
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Db 118 ACCTGCACGGTCTCTGATTTCTCATTAACCAAGAAATGCTTTAGGCTGGGTCGCCAGGCT 177
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QY 121 ccaggaagcgcttagtgtagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
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Db 178 CCAGAAAGCGCCGCGAGTGGGTGCTGTATACATATAGTGAAGTATAGGCTATTAAC 237
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QY 181 acagccctacagctcccgactccagcgtctcaccagggacccctccaaagcaattccctg 240
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Db 238 CCAGCCCTTAAGTCCCGCTCGCATCATCCAGGACACCTTCACAGAGTCAAGTCTCCCTG 297
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QY 241 tcactgcagcagctgactactagagacagggccattactactactgtgagc-----aaatc 294
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Db 298 TCACTGACGACGCTGACAGCTGAGGACGCCCATGTACTACTGTGCAAGATTAAGT 357
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QY 295 gtcactgtgacagctgtctcttactgtgttgactactgcgcagccagactctctacc 354
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Db 358 GGATGTGCTGCTGATGCTGTTGCTGTATGACACTAGTGGGCCAGAGACTCTGTCACC 417
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QY 355 gttctctca 363
||||| |||||||
Db 418 GTCTCTCA 426

RESULT 4
LOCUS OAVRB6IG 450 bp mRNA linear MAM 04-FEB-1998
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
(clone VRB6).
ACCESSION 249172
VERSION 249172.1 GI:794137
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 450)
AUTHORS Dufour,V.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
REFERENCE 2 (bases 1 to 450)
AUTHORS Dufour,V., Mallinge,S. and Nau,F.
TITLE The sheep Ig variable region repertoire consists of a single VH
family
JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
MEDLINE 96310953
FEATURES
source Location/Qualifiers
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31..>450
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GFSLSDAVNMVQAQKALEWVGIDNGGINTYNAALSKRLSITRDTSKQSVLSLS
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31..81
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82..450
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379..450
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/note="D-JH region"
BASE COUNT 99 a 139 c 116 g 96 t
ORIGIN

JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
MEDLINE 96310953
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/db_xref="taxon:9940"
/clone="VRA4"
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39..458
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/db_xref="GI:794126"
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/gene="VH"
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387..458
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D_segment
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BASE COUNT 97 a 140 c 123 g 98 t
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Best Local Similarity 80.7%; Pred. No. 2.6e-65;
Matches 293; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 cagggtgagctgcaggagtcggagaccagcctgtgtgaagccctcacagaccctctccctc 60
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DB 96 CAGGTGCACTGCAGAGAGTCGGAGCCAGCCTGTGAAGCCCTCACAGACCCTCTCCCTC 155
QY 61 acctgacaggtctctggtatctcaataaagaatgtgtgtgtgtgtgtgtgtgtgtgtgt 120
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DB 156 ACCTGACAGCGTTCTGATTCATTACCAAGCAATGCTGTACACATGGGGTCCCGCAGGCT 215
QY 121 ccaggaaagcgctgtgagtcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
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DB 216 CCGAGAAAGGTGCCGGAATGCTGGTGGTATGCGCACTGGTGGAGACACATTCATTAAG 275
QY 181 acagccctacagtcaccagctcagctcagcagagacactccaaagagccaattctccctg 240
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DB 276 CCGGCCCTAATGTCGGCGCTCAGCATCACAGGACAGCTCCAAAGCCAGCTCTCCCTG 335
QY 241 tcaactgacaggtgtgactgtgaggaacagggccaattactactgtgcgaatctgtcaat 300
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DB 336 TCACGTAGAGAGCTAACAAGTGAAGACGCGGTGTACTACTGTCAAGAAGATATCGAT 395
QY 301 ggtgacagtgcttcaatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
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DB 396 GGTACTGTGAATGTCTGGGATATCGAAACCTGGGGCCCAAGACTCTGTGTCACGTCTCC 455
QY 361 tca 363
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DB 456 TCA 458
RESULT 7
AF172680 369 bp mRNA linear MAM 01-SEP-1999
LOCUS AF172680
DEFINITION Ovis aries clone 146 immunoglobulin heavy chain precursor (IGHV)
MRNA, partial cds.
ACCESSION AF172680
VERSION AF172680.1 GI:5815228
KEYWORDS

SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
AUTHORS 1 (bases 1 to 369)
TITLE A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 369)
AUTHORS White G.P., Meusen, E.N.T. and Newton, S.E.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Center
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
FEATURES
source Location/Qualifiers
1..369
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="146"
/tissue_type="abomasal lymph node"
/note="Isolated from animals infected with Haemonchus
contortus"
1..369
/gene="IGHV"
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/product="immunoglobulin heavy chain precursor"
/protein_id="A4D52606.1"
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/translation="QVQLQSGPGLKPSQTLISCSVSGFSLTSYVYVVRQAPGKA
LEWVAIVYDMSKSYVPAKSRISVTRDSKSGVSLSVTTEQAVVYCARDRSV
YGHAYISDIWNGGLTVSS"
BASE COUNT 78 a 112 c 96 g 83 t
ORIGIN
Query Match 68.7%; Score 249.4; DB 4; Length 369;
Best Local Similarity 81.8%; Pred. No. 7.9e-65;
Matches 302; Conservative 0; Mismatches 61; Indels 6; Gaps 1;
QY 1 cagggtgagctgcaggagtcggagaccagcctgtgtgaagccctcacagaccctctccctc 60
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DB 1 CAGGTGCACTGCAGAGAGTCGGAGCCAGCCTGTGAAGCCCTCACAGACCCTCTCCCTC 60
QY 61 acctgacaggtctctggtatctcaataaagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
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DB 61 ACCTGCTCGGTCTGTGATTCATTACCAAGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ccaggaaagcgctgtgagtcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
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DB 121 CCGAGAAAGCACTGAGAGTGGTGGTGCATATATATGATGGAAGTGCATCTATAAC 180
QY 181 acagccctacagtcaccagctcagctcagcagagacactccaaagagccaattctccctg 240
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DB 181 CCGGCCCTGAATGCCGCTCAGCATCACAGGACAGCTCCAAAGCCAGCTCTCCCTG 240
QY 241 tcaactgacaggtgtgactgtgaggaacagggccaattactactgtgcgaatctgtcaat 300
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DB 241 TCACGTAGAGAGCTAACAAGTGAAGACGCGGTGTACTACTGTGTCAAGAAGATATCGAT 300
QY 301 ggtgacagtgcttcaatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 354
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DB 301 AGGTCTATGTGATCTGTATCTGTGCATGCACTACTAGGGGCCAGAGACTCTGTGTCAC 360
QY 355 gtctcctca 363
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DB 361 GTCTCTCA 369

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RESULT      8
LOCUS       OAVR41G
DEFINITION  OAVR41G 461 bp mRNA linear MAM 04-FEB-1998
            (clone VR4).
ACCESSION   Z49156.1 GI:794113
VERSION     249156.1
KEYWORDS    diversity region; immunoglobulin; immunoglobulin heavy chain;
            joining region; variable region.
SOURCE      sheep.
ORGANISM    Ovis aries
REFERENCE   1 (bases 1 to 461)
AUTHORS     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Caprinae; Ovis.
JOURNAL     Direct Submission
            Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
            1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
            2 (bases 1 to 461)
AUTHORS     Dufour V., Malinge, S. and Nau, F.
TITLE       The sheep Ig variable region repertoire consists of a single VH
            family
JOURNAL     J. Immunol. 156 (6), 2163-2170 (1996)
FEATURES
            source
            location/Qualifiers
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            sig_peptide
            V_region
            39..90
            90..461
            D_segment
            387..461
            /note="D-JH region"
            /product="VH region"
BASE COUNT  100 a 143 c 118 g 100 t
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Query Match 68.7%; Score 249.2; DB 4; Length 461;
Best Local Similarity 82.0%; Pred. No. 9e-65;
Matches 300; Conservative 0; Mismatches 63; Indels 3; Gaps 1;
QY 1 caagtcagctgcagagtcgagaccagcctgtgaagccctcacagacccttcctc 60
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DB 96 CAGGTGACGCTGCGAGAGTCGGAGCCCGCTGTGAGCCCTCAGACGACCTCTCCCTC 155
QY 61 acctgcaggtctctggtatctcatiaaccaaglatgltggttcggtccgcaagct 120
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DB 156 ACCTGCACGGTCTCTGATTCATTAAGCAGCAATTCATTTCGGGTCCGCCAGGCT 215
QY 121 ccaggaaggcgtctgagtgctcagtggtgtgtccagtggtgcactaacagcctatac 180
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DB 216 CCAAGAAAGGCACTGAGTGGGTGCTCTCATATTTAATGAAGAACACACCTATTAAC 275
QY 181 acagccttaagctccgagctcagcgtcacacaggaacacccccaagagccaattctccctg 240
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DB 276 CCGGCCCTGAATCCCGGATCAGCATACCGAGGACACCTCCAAAGCCAAAGTCTCCCTG 335
QY 241 tcaactaagcagcgtgactactagagacacgagccattactactgtcgaatctgtcaat 300
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DB 336 TCACTAGCAGCGCTGCACTAGAGACACGCGCATGTACTACTGTGAAATATTCGAAT 355
QY 301 ggtgacagtggtcctctatggttctg---gactactgagccagagactcctactaccctc 357
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DB 396 GCGGAGCGTTTGTGATGATGAGTGGGCGACTACTGAGGCGCCAGAGACTCTGTCCTCGTC 455
QY 358 tctctca 363
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DB 456 TCCTCA 461
RESULT      9
LOCUS       AF172674
DEFINITION  AF172674 366 bp mRNA linear MAM 01-SEP-1999
            Ovis aries clone 92 immunoglobulin heavy chain precursor (IGHV)
            mRNA, partial cds.
ACCESSION   AF172674
VERSION     AF172674.1 GI:5815217
KEYWORDS
SOURCE      sheep.
ORGANISM    Ovis aries
REFERENCE   1 (bases 1 to 366)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Caprinae; Ovis.
JOURNAL     White, G.P., Meusen, F.N.T. and Newton, S.E.
            A single-chain variable region immunoglobulin library from the
            abomasal lymph node of sheep infected with the gastrointestinal
            nematode parasite Haemonchus contortus
            Unpublished
            2 (bases 1 to 366)
AUTHORS     White, G.P., Meusen, F.N.T. and Newton, S.E.
TITLE       Direct Submission
            Submitted (26-JUL-1999) School of Veterinary Science, The Center
            for Animal Biotechnology, The University of Melbourne, Parkville,
            Melbourne, Victoria 3052, Australia
FEATURES
            source
            location/Qualifiers
            1..366
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            /clone="92"
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            /note="Isolated from animals infected with Haemonchus
            contortus"
            1..366
            /gene="IGHV"
            1..366
            /gene="IGHV"
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            /gene="IGHV"
            /codon_start=1
            /product="Immunoglobulin heavy chain precursor"
            /protein_id="AAD52601.1"
            /db_xref="GI:5815218"
            /translation="OYLOESGSLVYKPSQTLINCTVSGFSLFYNAVHWBQAGKY
            PMISISGSGSTYYNAALKSRSLITRDRSKQVSLSRVTEDSAVYYCASDDGDS
            VVDISIRHWGFGLVTVSS"
BASE COUNT  80 a 111 c 97 g 78 t
ORIGIN
Query Match 68.2%; Score 247.6; DB 4; Length 366;
Best Local Similarity 81.7%; Pred. No. 2.8e-64;
Matches 299; Conservative 0; Mismatches 64; Indels 3; Gaps 1;
QY 1 caagtcagctgcagagtcgagaccagcctgtgaagccctcacagacccttcctc 60
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DB 1 CAGGTGCACTGCGAGAGTCGGAGCCAGCTGTGTAAGCCCTCAGACAGACCTCTCCCTC 60
QY 61 acctgcaggtctctggtatctcatiaaccaaglatgltggttcggtccgcaagct 120
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DB 61 ACCTGCACGGTCTCTGATTCATTAACCTAACAATGCTGTACAGTGGGTCCGCCAGGCT 120
QY 121 ccaggaaggcgtctgagtgctcagtggtgtgtccagtggtgcactaacagcctatac 180
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DB 121 CCAAGAAAGTGCCTGCGAGTGGCTTGATGATGAGCAGTGGTGAAGCACATCTATAAT 180
QY 181 acagccttaagctccgagctcagcgtcacacaggaacacccccaagagccaattctccctg 240
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DB 181 GCGGCCCTGAATCCCGGCTCAGCATACCGAGGACACCTCCAAAGCCAAAGTCTCCCTG 240

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Oy	241	tcacgagcagcgtctacacgtgagacacgagccattctactctgtggca---aaccttc	297
Db	241	ttcactgagccgggtacacactgagacactggccgtgctactgtgcaaacgacgacgt	300
Oy	298	aatggtgcagctgtctccctactggtttgtgactactgagaccacagagactactacacgtc	357
Db	301	gatgtgtgttgacatatttctcattatctccactgacactgagccacgacactcctgtacacgtc	360
Oy	358	ttcctca	363
Db	361	ttcctca	366
RESULT 10			
LOCUS	OAVR21IG	449 bp	mRNA linear MAM 04-FEB-1998
DEFINITION	O.aries mRNA for immunoglobulin mu heavy chain variable region (clone VR21).		
ACCESSION	Z49166		
VERSION	Z49166.1	GI:794107	
KEYWORDS	diversity region; immunoglobulin; immunoglobulin heavy chain; joining region; variable region.		
SOURCE	sheep.		
ORGANISM	Ovis aries		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Caprinae; Ovis.		
AUTHORS	1 (bases 1 to 449)		
TITLE	Dufour V.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022		
AUTHORS	2 (bases 1 to 449)		
TITLE	Dufour V., Mallinge, S. and Nau, F.		
JOURNAL	The sheep Ig variable region repertoire consists of a single VH family		
MEDLINE	J Immunol. 156 (6), 2163-2170 (1996)		
FEATURES	96310953		
source	Location/Qualifiers		
gene	1..449		
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	SVSEEDTAMYYCVNRFSGKXWGYWGPGLVTVSS"		
	39..89		
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	/note="D-JH region"		
BASE COUNT	93 a 138 c 123 g 95 t		
ORIGIN			
Query Match	68.0%:	Score 247:	DB 4: Length 449:
Best Local Similarity	82.4%:	Pred. No. 4.2e-64:	
Matches 299: Conservative	0: Mismatches 55: Indels 9: Gaps 1:		
Oy	1	caggtgcagctgcagagatcgcggacccagcctggtgaagcctcacagacccctccctc	60

Db	Accession	Version	Source	Organism	Location/Qualifiers
Db	96	CAGGTGCGGCTCCAGAGATCGGAGCCCACTGTGTGAACCTTCACAGACCCCTTCCTC	155		
Qy	61	acctgcacggtctcgcgtatctcattcaaccaaatagggtgtagttgggtccgaaggt	120		
Db	156	ACCTGCACAGGTCCTCGGGCTTCATTAAACACACCTACAGTGAAGGCTGGGTCGCGAGCT	215		
Qy	121	ccaggaagaagcgctgagtgtgcttaggtgtgtgtcagtggtgcctaaagccataac	180		
Db	216	CCAGGAAGAAGCGCCTGAGTGGCTGTGTGTATGAAGAAATGATGATGTGCACAGCTATCAT	275		
Qy	181	acaagccctacaagctcccgactcagcgctcacacagagacacctccaaagccaattccctg	240		
Db	276	CCAGCCCTTAAGTCCCGGCTCAGCATCAACACAGAGACACCTCCAAAGAGCAAGTCCCTG	335		
Qy	241	tcactgagcagcggtgactactgaggaacagcgccattactactgtgcgaatctgcaat	300		
Db	336	TCACGACAGCAGCGGTACACAAGTAGAGACACGGCAATGACTACTGTGTAGAAAGTTTTC	395		
Qy	301	ggtagcagtgcttcctatggtgtgacactacgagacgagccagactcctaaccgtctcc	360		
Db	396	GGTGGAA-----AATACGTGGGGCTACTGTGGGCCACAGACCTCTGATCACCGTCTCC	446		
Qy	361	tca 363			
Db	447	TCA 449			
RESULT	11				
LOCUS	OAVRB1IG	447 bp	linear	MAM 04-FEB-1998	
DEFINITION	O.aries mRNA for immunoglobulin mu heavy chain variable region (clone VRB1).				
ACCESSION	Z49171				
VERSION	Z49171.1	GI:794133			
KEYWORDS	diversity region; immunoglobulin; immunoglobulin heavy chain; joining region; variable region.				
SOURCE	sheep.				
ORGANISM	Ovis aries				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.				
	1 (bases 1 to 447)				
REFERENCE	Dufour V.				
AUTHORS	Direct Submission				
TITLE	Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022				
JOURNAL	2 (bases 1 to 447)				
REFERENCE	Dufour V., Malinge S. and Nau F.				
AUTHORS	The sheep Ig variable region repertoire consists of a single VH family				
TITLE	J. Immunol. 156 (6), 2163-2170 (1996)				
JOURNAL	96310953				
MEDLINE					
FEATURES					
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	V-region	90..458 /gene="VH"
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Best Local Similarity	79.9%; Pred. No. 7.3e-64;	
Matches 290; Conservative	0; Mismatches 73; Indels 0; Gaps 0;	
Qy	1	cagtgacgcctgcaaggaaatcgaccacccgactgtgtgaagcctacaagaccttcctc 60
Db	96	CAGTGC GGCTGCAGAGATTGGGACC CCGCTGTGAAGCCCTCACAGACCTTCCTC 155
Qy	61	aactgcagcgtctcgtgatctccaataaacagaatgagtgtttgtgttcgccagagct 120
Db	156	AAC TGCAGAGGCTCTCGAATTCTCATTAACCAACTATGCTGCAGCGTGCTGCCAGGCT 215
Qy	121	ccaggaagaagcgcttagtgtagtgtagtgtgtgtccagtgtagtaacaaagcctataac 180
Db	216	CCAGGAAGAAGCGCGCTTGAA TGCTGTGATACATACTAATGAGGGGGAACCTTTAAC 275
Qy	181	acagccctcaagctcccgcagctacagctcaccaaggagaaacctcaagagcaatttcctc 240
Db	276	CAAGCCCTTAAGTCCC GCCCTCAGCACTAAACAGGGACACCTCCAAGAGCCAGGCTCCCTT 335
Qy	241	tcaactgagcagcgttacactacagagacacggccattactactgtgtcgaaatctgtcaat 300
Db	336	TCACTGAGACACGCGTGGCAGATGAGAGATACGGCCGCTGTCACTTGCTTTGGTAGT 395
Qy	301	ggtgacagtgttcctacttgattgtgactacttgaaacccagactcctaaccgctcc 360
Db	396	GGTGGCGCGCTGCTGATGGGATCGATCACTACGAGGGCC CAGAGATCTGTGCACCGCTGCC 455
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Db	456	TCA 458
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ACCESSION	AF172667	mRNA, partial cds.
VERSION	AF172667.1	GI:5815203
KEYWORDS		
SOURCE		
ORGANISM	Ovis aries	Sheep.
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprineae; Ovis.	
REFERENCE	1 (bases 1 to 366)	White,G.P., Meeußen,E.N.T. and Newton,S.E.

QY 358 tcctca 363
 Db 361 TCCTCA 366

RESULT 15

OVERLAPPING
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 DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
 (clone VR11)..
 ACCESSION 249158
 VERSION 249158.1 GI:794091
 KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
 joining region; variable region.
 SOURCE sheep.
 ORGANISM Ovis aries
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Caprinae; Ovis.
 1 (bases 1 to 458)

REFERENCE
 AUTHORS Dufour V.
 TITLE Direct Submission
 JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
 1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
 REFERENCE 2 (bases 1 to 458)
 AUTHORS Dufour V., Malinge S. and Nau F.
 TITLE The sheep Ig variable region repertoire consists of a single VH
 family
 JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
 MEDLINE 96310953
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 BASE COUNT 101 a 135 c 124 g 98 t
 ORIGIN

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 Best Local Similarity 81.4%; Pred. No. 8.4e-64;
 Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

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 Db 93 CAGGTGAGCTGCAGAGTGGAGCCAGCCTGCTGAGAGCCCTACAGACCTCTCCCTC 152

QY 61 acctgacggctctctgattctcaataaacaaglatggtgttagttggtcgcagagct 120
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 Db 153 ACCTGACAGGCTCTCTGATTCTCATTTAGTAACAATGCTCTAGAGCTGCGCAGGCT 212

QY 121 ccaggaaggcgcttgatgctagtgctggtgtgtccagtggtgcactaagcctataac 180

Db 213 CCAGAAAGACACTGGAGTGGGTAGGGAATATATGAGTGAATGAGATACATATATAAC 272
 |||||||
 QY 181 acagcctacagtcaggactccgactcagcgtcacacagagagacactccaagagccaatctccctg 240
 |||||||
 Db 273 CCGGCCCTGAATCCCGGCTCAGCATCACAGGACACTCCAAAGCCAAAGTGTCCCTG 332

QY 241 tcactgacagcgtgactactgagacacagcggccattactactgtgcgaatctgcaat 300
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 Db 333 TCAGTGACGAGCGTATCAATGTGACGACAGGCGCGTCTACTACTGTGCAGAGATGAGANT 392

QY 301 ggtgac---agtgctccctatggtgttgactactggaagccagagactcctactacgctc 357
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 Db 393 AGTGGCTGGACTTATGTGGGAGGTATCGACTACTGGGCGCAGGACTCCTGTGTACCGTTC 452

QY 358 tcctca 363
 Db 453 TCCTCA 458

Search completed: August 11, 2002, 22:03:49
 Job time: 8214 sec

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Tue Aug 13 08:57:19 2002

OM of: US-09-786-015-2 to: EST:* out_format: pfs
Date: Aug 12, 2002 10:07 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-O/cgnt2_1/USPFO.spool/US09786015/runatc_12082002_092422_40/app_query.fasta.1.347
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-MIMATCH=0.050 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
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-LIST=7.000 -START=1 -MATRIX-biosum62 -TRANS-human40.cdf
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM-ext -HEAPSIZE=300
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Search information block:

Query: US-09-786-015-2
Query length: 121
Database: EST:*
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 2544.760000

Score list:

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gb_est2:BE846229	+	447.50	877.11	579	BE846229 232099 BARC 5BOV Bos
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gb_est2:BE606302	+	438.00	859.97	495	BE606302 273305 MARC 3BOV Bos
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gb_est2:BE484853	+	427.00	838.08	498	BE484853 171651 BARC 5BOV Bos
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gb_est2:BE688447	+	426.50	836.76	513	BE688447 336072 BARC 5BOV Bos
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gb_est2:BE845785	+	420.50	824.99	507	BE845785 232825 BARC 5BOV Bos
gb_est2:BE487664	+	420.00	823.95	509	BE487664 176725 BARC 5BOV Bos
gb_est2:BE688665	+	419.00	819.59	637	BE688665 336371 BARC 5BOV Bos
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gb_est2:BE689490	+	414.00	812.24	500	BE689490 337581 BARC 5BOV Bos

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gb_est2:BE588428 + 413.50 809.28 7.9e-36 599 BE588428 194011 BARC 5BOV Bo
gb_est2:BE487301 + 413.00 810.17 7.0e-36 504 BE487301 175972 BARC 5BOV Bo
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DEFINITION 167909 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
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VERSION BE482206.1 GI:9601739
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 476)
Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8416

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

Small pass sequencing. Bases called and alt trimmed with phred
v0.98004.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR PRIMERS
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BACKWARD: GTTTCCTGACGACGAC
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Location/Qualifiers
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/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPOR6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

FEATURES

source

BASE COUNT 98 a 134 c 143 g 101 t
ORIGIN

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Quality: 448.00 Length: 130
Ratio: 4.110 Gaps: 2
Percent Similarity: 83.846 Percent Identity: 71.538

alignment_block:

US-09-786-015-2 x BE482206 ..
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13 CAGGTGAGTGGCGGAGTGGCGCCAGCTGTGAAGCCCTCAGAC 62
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysGly 34
|||||
63 CCGTCCCTACCGCAGCGGTCTGTGATTCCTATTGACGACGATG 112
34 aISerrPValArgGlnAlaProGlyLysAlaLeuGlnTrrPLeuGly 50

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163 ATAGATGATGGTGGAGACACAGCCTATATCCAGCCTGAAATCCCGGCT 212
67 uSerValThrArgAspThrSerIlySerGlnPheSerLeuSerLeuSer 84
213 CACATCACCAGCAAGCAACTCCAAAGACCAGTCTCTCTGCTCACTAGCA 262
84 erValThrThrGluAspThrAlaAlaLeuTyrCysAlaIlySerValAsn 100
263 GCGTGACAACTGAGACGCGCCACATCTACTGTGCGAAAAAAGTGGT 312
101 G1yAspSerValProTyrGly.....Le 108
313 GGTGGT.....TATGCTGTGGTGGAGGCGTCCATTTATGATTACGT 353
108 uAspTyrTrpSerProGlyLeuLeuThrValSerSer 121
354 CGATGCTCGGCGCAAGACTCCTGTCACCGTCTCCTCA 393
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DEFINITION 232099 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE846229
VERSION BE846229.1 GI:10283053
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 579)
Sontegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
Contact: Sontegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing: Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGACGACGAG
Plate: 112 row: J column: 9
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FEATURES
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Location/Qualifiers

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/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
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tissues at eight physiological, developmental, and disease
states."
BASE COUNT 108 a 171 c 166 g 134 t
ORIGIN

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alignment_scores:
Quality: 447.50 Length: 134

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Ratio: 4.106 Gaps: 1
Percent Similarity: 81.343 Percent Identity: 68.657
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US-09-786-015-2 x BE846229 ..
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114 CCTCTCCCTCACCCTGCACGGCTCTCTGATTCTCATTTGACGACGATCTG 163
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164 TAGGCTGGTCCGCGAGCTCCGGGAGGCGCTGGAGTGGTGGTGGT 213
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
214 ATAGATGATGGTGGAGACATACATGCTTATTTAGCCCTGCAATCCCGCT 263
67 uSerValThrArgAspThrSerIlySerGlnPheSerLeuSerLeuSer 84
264 CAGATCACCAGCAAGCAACTCCAAAGACCAGTCTCTCTGCTCACTAGCA 313
84 erValThrThrGluAspThrAlaAlaLeuTyrCysAlaIlySer..... 98
314 GCGTGACAACTGAGACGCGCCACATCTACTGTGCGAAAAAAGTGG 363
99 .....ValAsnGlyAspSerVal 104
364 GGTTTTATGTTATGCTCTTATGTTGCTGTGTTATGTTATGTTATGTTA 413
104 lProTyrGlyLeuAspTyrTrpSerProGlyLeuLeuThrValSer 121
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DEFINITION 195790 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE589545
VERSION BE589545.1 GI:9842584
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 505)
Sontegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
Contact: Sontegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing: Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers

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TITLE
JOURNAL
COMMENT

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FORWARD: AGGAACAGCTATGACCAT
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 Seq primer: ATTAGTGACACTATAG.

FEATURES
 source Location/Qualifiers

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 /tissue_type="pooled"
 /lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

BASE COUNT 111 a 149 c 138 g 107 t
 ORIGIN

alignment_scores:

Quality: 444.50 Length: 123
 Ratio: 4.154 Gaps: 2
 Percent Similarity: 86.992 Percent Identity: 73.984

alignment_block:

US-09-786-015-2 x BE589545 ..

Align seg 1/1 to: BE589545 from: 1 to: 505

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17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyGly 34
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130 CCTCTCCTCCTACCTGACGAGCTCTGTGATTCTCTTGAAGCACTATCTTG 179
34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
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51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArg 67
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67 userValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
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84 erValThrThrGluAspThrAlaIleTyrTyrcysAlaLysSerValAsn 100
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330 GCGTGACACTGAGACAGCGCCACATACCTGTCGAAGGCTTATAT 379
101 GlyAspSer.....ValProTyrglyLeuAspTyrTrpSerProGly 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
380 GGATGATGTGGGATTAATATGTT...GATGCTGGGGGCCAGACT 426
115 uLeuLeuThrValSerSer 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
427 CTTGGTACCGTCTCTCA 445

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seq_name: gb_est2:BE480296

seq_documentation_block:

LOCUS BE480296 514 bp mRNA linear EST 28-AUG-2000
 DEFINITION 165337 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE480296
 VERSION BE480296.1 GI:9599829

KEYWORDS EST.
 SOURCE
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

REFERENCE
 1 (bases 1 to 514)
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Bovidae; Bovinae; Bos.
 1 (bases 1 to 514)
 Sontegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
 Wells, K.D.
 Mapping of Expressed Sequence Tags from a normalized bovine mammary
 gland cDNA library
 Unpublished (2000)
 Contact: Sontegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2N, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@lpsl.barc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross-match with the -minscore 18
 and -mismatch 12 options.

PCR PRIMERS
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACGACGACG
 Plate: 16 row: D column: 1
 Seq primer: ATTAGTGACACTATAG.

FEATURES

source Location/Qualifiers

1..514
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BARC 5BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

BASE COUNT 103 a 161 c 137 g 113 t
 ORIGIN

alignment_scores:

Quality: 441.50 Length: 128
 Ratio: 4.088 Gaps: 2
 Percent Similarity: 84.375 Percent Identity: 72.656

alignment_block:

US-09-786-015-2 x BE480296 ..

Align seg 1/1 to: BE480296 from: 1 to: 514

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1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
75 CAGGTGACGTCGCGGAGTCCGGCCAGCCTGTGTAAGCACTATCTTG 124
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyGly 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 CCTCTCCTCCTACCTGACGAGTCTGTGATTCTCTTGAAGCACTATCTTG 174
34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
175 TATCCTGGTCGCGCAGCGCTCCAGGAAAGCGCTGAGATGCTTGGTAT 224
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArg 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
225 GTAAGTGTGTGGGAGACACAGCTATATACCCACGCTGAATCCCGCT 274
67 userValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
275 CAGATTCACCAAGACACTCCAGAGCCAGACTCTCTGTGCTGAGTGA 324
84 erValThrThrGluAspThrAlaIleTyrTyrcysAlaLysSerValAsn 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
325 GCGTTACAACTGATGACAGCGCCACCTACTACTGTGCGAAGCTTACG 374
101 GlyAspSerVal.....ProTyrglyLeuAspTyr..... 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
375 GCTGTGACCGCTACTATGATGTTGCTTATGTTATGATGATGATGATG 424

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111 .TrpSerProGlyLeuLeuLeuThrValSerSer 121
||||: ||||||:|||||
425 CTGGGGCCAAAGACTCCTGGTCACCGCTCTCTCA 458

seq_name: gb_est2:BF606302

seq_documentation_block:
LOCUS      BF606302                495 bp    mRNA    linear    EST 25-APR-2001
DEFINITION 273305 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BF606302
VERSION     BF606302.1  GI:11706773
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 495)
            Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Keefe,J.W., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
            .
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
21180013
COMMENT    Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -mnscore 18
            and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 60 row: G column: 12
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
            source
            1..495
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone_lib="MARC 3BOV"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /note="Vector: PCMV SPORF6; Site_1: XbaI; Site_2: XhoI;
            library made from pooled tissue from marrow, alveolar
            macrophage, ovary, fetal semitendinosus muscle, and fetal
            longissimus muscle."
BASE COUNT  104 a 152 c 128 g 111 t
ORIGIN
alignment_scores:
            Quality: 438.00      Length: 127
            Ratio: 4.093        Gaps: 2
Percent Similarity: 84.252      Percent Identity: 71.654

alignment_block:
US-09-786-015-2 x BF606302 ..
Align seg 1/1 to: BF606302 from: 1 to: 495

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||
79 CAGGTGACCTGCGCGGAGTCGGGCCAGCCTGTGAAGCCCTCACAGAC 128
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrgly 34
|||||:|||||:|||||:|||||:|||||:|||||

```

```

129 CCTCTCCCTGACCTGCAGACGACCTGTGATTCTATTGAGCGCCTATACTA 178
34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnGlyLeuGly 50
|||||:|||||:|||||:|||||:|||||:|||||
179 TAGCCTGGGTCGCCAGGCTCCGGGGAAGGCGCTGGAGTGGCTTGGTGT 228
51 ValSerSerGlyAlaLeuThrAlaTyraAsnThrAlaLeuGlnSerArg 67
|||||:|||||:|||||:|||||:|||||:|||||
229 ATAGTAGTGGGGAAGACATGCTTAACCCAGCCCTGGAATCCGGCT 278
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||:|||||:|||||:|||||:|||||:|||||
279 CAGGTCACCAAGACACTCCAGAGCAAGTTCTCTGTCACTTAGCA 328
84 erValThrThrGluAspThrAlaLeuTyrcysAlaLysSer...Val 99
|||||:|||||:|||||:|||||:|||||:|||||
329 GCATGACACACTGAGACACGCGCCACATACACTGTGCGAAGGCTTGT 378
100 AsnGlyAspSerVal.....ProTyrglyLeuAspTyrrTr 111
|||||:|||||:|||||:|||||:|||||:|||||
379 AATGGATCCTAATAGTGTGTTTATGATGTATATCACTGATGCTG 428
111 pSerProGlyLeuLeuLeuThrValSerSer 121
|||||:|||||:|||||:|||||:|||||:|||||
429 GGGCCAAAGACTCCTGGTCACCGCTCTCTCA 459

seq_name: gb_est2:BE485907

seq_documentation_block:
LOCUS      BE485907                502 bp    mRNA    linear    EST 28-AUG-2000
DEFINITION 173199 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE485907
VERSION     BE485907.1  GI:9605440
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 502)
            Sontegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
            Wells,K.D.
            Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
            Unpublished (2000)
COMMENT    Contact: Sontegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@lpsl.barc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -mnscore 18
            and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 131 row: G column: 6
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
            source
            1..502
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone_lib="BARC 5BOV"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /note="Vector: PCMV SPORF6; Site_1: XbaI; Site_2: XhoI;
            library made from pooled mRNA isolated from mammary
            tissues at eight physiological, developmental, and disease
            states."
BASE COUNT  109 a 154 c 129 g 110 t
ORIGIN

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alignment_scores:

Quality: 434.00 Length: 130
Ratio: 3.945 Gaps: 2
Percent Similarity: 84.615 Percent Identity: 68.462

alignment_block:

US-09-786-015-2 x BE485907 ..

Align seg 1/1 to: BE485907 from: 1 to: 502

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1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 CAGGTGACACTGGCGGAGTCGGGCCCCAGCGTGTGAAGCCCTCACAGAC 127
17 rLeuSerLeuThCysThValSerGlyPheSerLeuThrLysTyGly 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
128 CCTCTCCCTCACCTGCACGCTCTCTGATTCTCATTAAGCAGCTATGCTG 177
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 TAAGTGGGTCCGCCAGGCTCCAGGGAAGGCGCTGAGTGCCTCGGTGCT 227
51 ValSerSerGlyAlaLeuThrAlaTyAsnThrAlaLeuGlnSerArgle 67
:::|||||:|||||:|||||:|||||:|||||:|||||:
228 ATAACTAGTGTGAGTACAGACTATTAAGCTGAGCCCTGAATTCGGGCT 277
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
278 CAGCATCCACCAAGACACTCCAAAGCCAAAGTCTCTGTCTGAGTACGA 327
84 erValThrThrGluAspThrAlaIleTyTyrcysAlaLysSerValasn 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 GCCTGACACTGAGGACAGCGCCACATCTCTGTGCTCAAAAAAACAAC 377
101 .....GlyAspSerValProTyGly 108
|||||:|||||:|||||:|||||:|||||:|||||:
378 AATGTTAATACTGTGAATTGTGTGTGTGAGTACGATGACACTAC...GT 424
108 uAspTyTrpSerProGlyLeuLeuLeuThrValSerSer 121
:::|||||:|||||:|||||:|||||:|||||:|||||:
425 CGATGCTGTGGGCCAAGACTCTGTGTACCCGTCTCTCA 464
```

seq_name: gb_est2:BE845758

seq_documentation_block:

LOCUS BE845758 549 bp mRNA linear EST 25-SEP-2000
DEFINITION 232868 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE845758
VERSION BE845758.1 GI:10282582

KEYWORDS

EST.

SOURCE

cow.

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 549)

AUTHORS

Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and

TITLE

Mapping of Expressed Sequence Tags from a normalized bovine mammary

JOURNAL

gland cDNA library

COMMENT

Unpublished (2000)

Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psl.barc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -m1nscore 18

and -mismatch 12 options.

PCR primers

FORWARD: AGCAACAGCTATGACCAT

BACKWARD: GTTTCACGACGACG

Plate: 113 row: j column: 9

Seq primer: ATTTAGTGACCTATGAT.

Location/Qualifiers

1. 549

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="BARC 5BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPOR6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states."

BASE COUNT

114 a 167 c 151 g 117 t

ORIGIN

alignment_scores:

Quality: 434.00 Length: 128
Ratio: 4.019 Gaps: 3
Percent Similarity: 84.375 Percent Identity: 71.094

alignment_block:

US-09-786-015-2 x BE845758 ..

Align seg 1/1 to: BE845758 from: 1 to: 549

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1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 CAGGTGACACTGGCGGAGTCGGGCCCCAGCGTGTGAAGCCCTCACAGAC 127
17 rLeuSerLeuThCysThValSerGlyPheSerLeuThrLysTyGly 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
128 CCTCTCCCTCACCTGCACGCTCTCTGATTCTCATTAAGCAGCTATGCTG 177
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 TAAGTGGGTCCGCCAGGCTCCAGGGAAGGCGCTGAGTGCCTCGGTGCT 227
51 ValSerSerGlyAlaLeuThrAlaTyAsnThrAlaLeuGlnSerArgle 67
:::|||||:|||||:|||||:|||||:|||||:|||||:
228 ATAAACAGTGTGTGAAGCACAGCTATTAACCCAGCCCTGAATTCGGGCT 277
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
278 CAGCATCCACCAAGACACTCCAAAGCCAAAGTCTCTGTGCTGAGTACGA 327
84 erValThrThrGluAspThrAlaIleTyTyrcysAlaLysSer..... 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 GCCTGACACTGAGGACAGCCACATCTACTGTGCAAAAAAATTGTGAT 377
99 .....ValasnGlyAspSerValProTy.....GlyLeuAspTy 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 AGGTGCTGTGTGTGAT...TATAGTTATCTGTGTCGGGACAAAGATGC 424
110 rTrpSerProGlyLeuLeuLeuThrValSerSer 121
:::|||||:|||||:|||||:|||||:|||||:|||||:
425 CTGGGCCAAGGACTCTTACTGACCGTCTCTCA 458
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seq_name: gb_est2:BE476735

seq_documentation_block:

LOCUS BE476735 489 bp mRNA linear EST 28-AUG-2000
DEFINITION 160120 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE476735
VERSION BE476735.1 GI:9596268

KEYWORDS

EST.

SOURCE

cow.

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 489)
 Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and Wells,K.D.
 TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Sonstegard TS
 USA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGCAGCAGC
 Plate: 28 row: J column: 21
 Seq primer: ATTGAGTGACCTATGAC.
 FEATURES
 source 1..489
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BARC 5BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
 BASE COUNT 107 a 150 c 128 g 104 t
 ORIGIN
 alignment_scores:
 Quality: 433.50 Length: 121
 Ratio: 4.051 Gaps: 1
 Percent Similarity: 88.430 Percent Identity: 72.727
 alignment_block:
 US-09-786-015-2 x BE476735 ..
 Align seg 1/1 to: BE476735 from: 1 to: 489
 1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValysProSerGlnth 17
 |||||
 82 CAGGTGACGTGGCGGAGTGGGCGCCAGCGCTGTGAAGCCCTCAGAC 131
 17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrlsTygIyV 34
 |||||
 132 CCGTCCCTCAGCTGACGGGTCTGTGATTCTCATTAAGCATATATG 181
 34 alSerTrpValArgGlnAlaProGlyLysAlaLeuGlnuTrpLeuGlyGly 50
 |||||
 182 TAAACTGGTGGCCGACAGCTCCAGAAAGCGCTGGAGTGGCTGGGTG 231
 51 ValSerSerGlyAlaLeuThrlaTyAsnThrlAlaLeuGlnSerArgle 67
 :::::
 232 ATTAAGAGTGGTGAAGCAGCGCTATTAACCCAGCCCTGAATCCGGCT 281
 67 uSerValThrArgAspThrSerIysSerGlnPheSerLeuSerLeuSers 84
 |||||
 282 CAGCATCCACCAAGAGCAACATCAAGAGCCAGTCTCTCGGTGAGCA 331
 84 erValThrThrGlnuAspThrAlaAlaIleTyTrcysAlaIysSerValAsn 100
 |||||
 332 GCGGTGACCTGAGGACACAGCACAATACACTGTGTGAAGAGTTGGT 381
 101 GlnAspSerValProTyrgIyLeuAspTyTrpSerProGlyLeuLeu 117
 |||||
 382 GGATATAGTACT...TATACATATATACCTGGGGCCAGGACTCTGCT 428

117 urhValSerSer 121
 :|||||
 429 CACCGTCTCCTCA 441
 seq_name: gb_est2:BE588903
 seq_documentation_block:
 LOCUS BE588903 595 bp mRNA linear EST 28-AUG-2000
 DEFINITION 194569 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE588903
 VERSION BE588903.1 GI:9841942
 KEYWORDS EST.
 SOURCE Cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 595)
 Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and Wells,K.D.
 TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Sonstegard TS
 USA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGCAGCAGC
 Plate: 121 row: C column: 10
 Seq primer: ATTGAGTGACCTATGAC.
 FEATURES
 source 1..595
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BARC 5BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
 BASE COUNT 119 a 178 c 167 g 131 t
 ORIGIN
 alignment_scores:
 Quality: 433.00 Length: 133
 Ratio: 3.936 Gaps: 3
 Percent Similarity: 82.707 Percent Identity: 67.669
 alignment_block:
 US-09-786-015-2 x BE588903 ..
 Align seg 1/1 to: BE588903 from: 1 to: 595
 1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValysProSerGlnth 17
 |||||
 64 CAGGTGACGTGGCGGAGTCAAGGCCAGCGCTGTGAAGCCCTCAGAC 113
 17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrlsTygIyV 34
 |||||
 114 CCGTCCCTCAGCTGACGGGTCTGTGATTCTCATTAAGCATATATG 163
 34 alSerTrpValArgGlnAlaProGlyLysAlaLeuGlnuTrpLeuGlyGly 50
 |||||
 164 TAAACTGGTGGCCGACAGCTCCGGAAGCAGCTGAGTGGGTGGGT 213


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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC SBOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

BASE COUNT      109 a      150 c      149 g      110 t
ORIGIN

alignment_scores:
  Quality:      430.50      Length:      134
  Ratio:        3.950      Gaps:        3
  Percent Similarity: 81.343      Percent Identity: 68.657

alignment_block:
  US-09-786-015-2 x BE476121 ..

Align seg 1/1 to: BE476121 from: 1 to: 518

1 GlnValGlnLeuGlnGluSerGlyProSerLeuValLysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 CAGGTGCAGCTGCCGAGCTGGGCCCGACCTGGTGAAGCCCTCACAGAC 146
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrgly 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
147 CCTCTCCTCCTACCTGACAGCGTCTGTGATCTCATTTGAGCAGTATGCTG 196
34 alserTrrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
197 TAAGCTGGATCGCCAGCTCTCAGGGAAGGCGCTGAGTGGCTGGTGT 246
51 ValSerSerGlyAlaLeuThralaTyraThrAlaLeuGlnSerArgLe 67
::: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
247 ATACAGATGGTGGAGACACAGCGCTATTAACCCACCCCGAATCCGGCT 296
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
297 CAGCATCCACCAAGCAACACTCCAAAGAGCCAGTCTCGCTGACATGAGACA 346
84 erValThrThrGluAspThrAlaIleTyryCysAlaLysSerVal... 99
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
347 GCGTGACACCTGAGACACGCGCACATACCTGTGCAAAAAGTTCTTAT 396
100 .....AsnGlyAspSer.....ValProTyrgly..... 107
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
397 GGTGTGTGGTGGCATAGTGTGTAAGTGTGGCTTATGGTCATGTTA 446
108 .....LeuAspTyrrTpSerProGlyLeuLeuLeuThrValSerS 121
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
447 TAGGACATACGTCGATCGCTGGGCGCAAGACACTCTGTGTCACCGCTCT 496
121 er 121
||
497 CA 498

seq_name: gb_est2:BG692944

seq_documentation_block:
LOCUS      BG692944      513 bp      mRNA      linear      EST 02-MAY-2001
DEFINITION  342818 BARC SBOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BG692944
VERSION    BG692944.1 GI:13934764
KEYWORDS   EST.
SOURCE     EST.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 513)

```

```

AUTHORS      Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
              Wells,K.D.
TITLE        Mapping of Expressed Sequence Tags from a normalized bovine mammary
              gland cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Sonstegard TS
              USD, ARS, Beltsville Agricultural Research Center
              Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
              Tel: 301 504 8416
              Fax: 301 504 8416
              Email: tads@psi.barc.usda.gov
              Single pass sequencing. Bases called and alt trimmed with phred
              v0.980904.e. Vector identified by cross-match with the -minscore 18
              and -mismatch 12 options.
PCR Primers  FORWARD: AGGAACAGCATATGACAC
              BACKWARD: GTTTCCTCAGTACGACG
              Plate: 43 row: J column: 13
              Seq primer: ATTAGCTACACATATAG.
              Location/Qualifiers
                1..513
                  /organism="Bos taurus"
                  /db_xref="taxon:9913"
                  /clone_lib="BARC SBOV"
                  /tissue_type="pooled"
                  /lab_host="DH10B"
                  /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                  Library made from pooled mRNA isolated from mammary
                  tissues at eight physiological, developmental, and disease
                  states."

BASE COUNT      106 a      155 c      139 g      113 t
ORIGIN

alignment_scores:
  Quality:      428.00      Length:      133
  Ratio:        3.891      Gaps:        3
  Percent Similarity: 82.707      Percent Identity: 69.925

alignment_block:
  US-09-786-015-2 x BG692944 ..

Align seg 1/1 to: BG692944 from: 1 to: 513

1 GlnValGlnLeuGlnGluSerGlyProSerLeuValLysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 CAGGTGCAGCTGCCGAGCTGGGCCCGACCTGGTGAAGCCCTCACAGAC 113
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrgly 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
114 CCTCTCCTCCTACCTGACAGCGTCTGTGATCTCATTTGAGCAGCTATGCTG 163
34 alserTrrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
164 TAAGCTGGTCCGCCAGGCTCCAGGGAAGGCGCTGAGTGGCTCGAGGT 213
51 ValSerSerGlyAlaLeuThralaTyraThrAlaLeuGlnSerArgLe 67
::: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
214 ATTCGACATAGTGAACACACAGCTATTAACCCACCCCGAATCCGGCT 263
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
264 CAGCATCCACCAAGCAACCTCCAAAGAGCAGTCTGTGTCAGTGAACA 313
84 erValThrThrGluAspThrAlaIleTyryCysAlaLysSer..... 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
314 GCGTGACACCTGAGACACGCGCACATACCTGTGCAAAAAGTATAT 363
99 .....ValAsnGlyAspSerValPro.....Tyrgly.. 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 AGTGTGGCGGTGTGGTGTGGTGTGTGTGTGTGTGTGTATATATGAGTAA 413
108 .....LeuAspTyrrTpSerProGlyLeuLeuLeuThrValSerS 121

```



```

alignment_block:
US-09-786-015-2 x BE480721 ..
Align seg 1/1 to: BE480721 from: 1 to: 509

1 GluValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||.....
91 CAGGTGACGCTGCGGAGTCGGGCCCAAGCTGTGTGAAGCCCTCACAGAC 140
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTrgIly 34
|||||.....
141 CCTCTCCCTCACCTGCACGGTCTGTGATCTCTATTAAGCAGCATATATG 190
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
|||||.....
191 TAGGCTGGGTCCGCGCAGCTCCAGGAAAGGGCTAGATAGCTCTGCTGTC 240
51 ValSerSerGlyAlaLeuThrAlaTyraThrAlaLeuGlnSerArgIle 67
|||.....
241 ATACATAGTGTGGAAACACACAGACTATACCCGCCCTGAATGCGGCT 290
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|.....
291 CATCATCACCAGAGACAACCTCCAGAGCACAAGCTCTCTATCACTGAGCA 340
84 eValThrThrGluAspThrAlaIleTyrTrpCysAlaLysSerValAsn 100
|||||.....
341 GCGGACACACTGAGACACGCGCACATCACTGTGCAGATGTATTAT 390
101 GLYASP.....SerValProTyrGlyLeuAspTyrTrpSerProGlyIle 115
|||||.....
391 GGTATGTTATTTCTTGAATTTCTCTGTGGAC...TGGGCGCAGGACT 437
115 uLeuLeuThrValSerSer 121
|||||.....
438 CCTGGCACCGCTCTCCCA 456

seq_name: gb_est2:BE588530

seq_documentation_block:
LOCUS BE588530 581 bp mRNA linear EST 28-AUG-2000
DEFINITION 193837 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE588530
VERSION BE588530.1 GI:9841569
KEYWORDS EST.
SOURCE
COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 581)
Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
CONTACT: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 116 row: D column: 22
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1..581
/organism="Bos taurus"

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/dB_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCWV SPORF6; Site.1: XbaI; Site.2: XhoI;
library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

BASE COUNT 112 a 174 c 169 g 126 t
ORIGIN

alignment_scores:
Quality: 427.50 Length: 132
Ratio: 3.958 Gaps: 2
Percent Similarity: 81.818 Percent Identity: 68.182

alignment_block:
US-09-786-015-2 x BE588530 ..
Align seg 1/1 to: BE588530 from: 1 to: 581

1 GluValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||.....
61 CAGGTGACGCTGCGGAGTCGGGCCCAAGCTGTGTGAAGCCCTCACAGAC 110
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTrgIly 34
|||||.....
111 CCTCTCCCTCACCTGCACGGTCTGTGATCTCTATTAAGCAGCATATATG 160
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
|||||.....
161 TAACTGGGTCCGCGCAGCTCCAGGAAAGGGCTGAGTGTCTGCTGTGT 210
51 ValSerSerGlyAlaLeuThrAlaTyraThrAlaLeuGlnSerArgIle 67
|||.....
211 ATACAGAGTGTGGAAACACACAGCTATACCCAGCCCTGAATGCCGCT 260
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|.....
261 CAGCATCACCAGAGACAACCTCCAGAGCACAAGCTCTCTGATCACTGAGCA 310
84 eValThrThrGluAspThrAlaIleTyrTrpCysAlaLysSerValAsn 100
|||||.....
311 GCGGACACACTGAGACACGCGCACATCACTGTGCAGAAAGCTGTGT 360
101 GLYASP.....SerVal.....ProTyrGlyLeuAs 109
|||.....
361 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCA 410
109 pTyr.....TrpSerProGlyLeuLeuLeuThrValSerSer 121
|||||.....
411 TTACGTGATGCTCGGGGCCAAGACATCTGTGTACCGCTCTCCCA 456

```

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2002, 09:25:38 ; Search time 52.21 seconds
(without alignments)
236.146 Million cell updates/sec

Title: US-09-786-015-4

Perfect score: 564

Sequence: 1 QDVLQTGSVSSVSGSLGQRVSI.....SYQSYSGVFGSGRLTVLG 111

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_032802:*
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564	100.0	111	21	AAV82529
2	389	69.0	147	22	AAV82529
3	388.5	68.9	236	22	AAV82529
4	387	68.6	249	22	AAV82529
5	386	68.4	110	22	AAV82529
6	385.5	68.4	109	22	AAV82529
7	385	68.3	113	22	AAV82529
8	385	68.3	117	22	AAV82529
9	383.5	68.0	112	21	AAV82529
10	382	67.7	111	22	AAV82529
11	382	67.7	249	21	AAV82529

12	381.5	67.6	246	21	AAV82529
13	381	67.6	110	22	AAV82529
14	381	67.6	111	22	AAV82529
15	381	67.6	111	22	AAV82529
16	381	67.6	113	22	AAV82529
17	381	67.6	235	22	AAV82529
18	380.5	67.5	130	22	AAV82529
19	380	67.4	111	18	AAV82529
20	380	67.4	111	20	AAV82529
21	380	67.4	111	20	AAV82529
22	379.5	67.3	131	21	AAV82529
23	379.5	67.3	112	18	AAV82529
24	379.5	67.3	118	22	AAV82529
25	379.5	67.3	242	21	AAV82529
26	379	67.2	235	22	AAV82529
27	379	67.2	251	22	AAV82529
28	378.5	67.1	112	21	AAV82529
29	377	66.8	110	22	AAV82529
30	377	66.8	111	15	AAV82529
31	377	66.8	111	18	AAV82529
32	377	66.8	249	20	AAV82529
33	377	66.8	258	18	AAV82529
34	377	66.8	262	20	AAV82529
35	376.5	66.8	310	20	AAV82529
36	376	66.7	110	20	AAV82529
37	376	66.7	110	20	AAV82529
38	376	66.7	110	20	AAV82529
39	376	66.7	110	20	AAV82529
40	376	66.7	110	20	AAV82529
41	376	66.7	110	20	AAV82529
42	376	66.7	111	20	AAV82529
43	375	66.5	110	21	AAV82529
44	375	66.5	132	22	AAV82529
45	375	66.5	242	20	AAV82529

ALIGNMENTS

RESULT 1	AAV82529	standard; Protein; 111 AA.
ID	AAV82529	
AC	AAV82529	
XX		
DT	13-JUL-2000	(first entry)
XX		
DE	Carcinoembryonic antigen affinity antibody light chain variable region.	
XX		
KW	Carcinoembryonic antigen; CEA; sheep; monoclonal antibody; tumour associated antigen; anti-carcinogenic; cytostatic; cancer therapy.	
XX		
OS	Ovis sp.	
XX		
PN	WO200012556-A1.	
XX		
PD	09-MAR-2000.	
XX		
PF	20-AUG-1999;	99WO-GB02729.
XX		
PR	28-AUG-1998;	98GB-0018915.
XX		
PA	(KSBI-) KS BIOMEDIX LTD.	
XX		
PI	Harrison PJ;	
XX		
DR	WPI; 2000-375618/32.	
XX		
DR	N-PSDB; AAA08401.	
XX		
PT	A new high-affinity monoclonal antibody that is characterized by an acid-washed enzyme-linked immunosorbent assay for use in cancer therapy	
XX		

Internalising anti
Anti-idiotype mon
Amino acid sequenc
Anti-IL-18 antibod
Human Vlamdai-1-1
Anti-IL-18 antibod
Light chain sequen
Anti-melanoma ligh
VL domain CDR of a
M4H7 Mab light ch
Anti-Platelet glyc
C6 human sfv antib
Amino acid sequenc
Anti-platelet glyc
Human immune syste
Novel human diagn
Anti-IL12 antibody
Human autoantibody
Monoclonal antibod
C6 human sfv antib
Antibody 10F6 sing
C6 human sfv antib
C6.5/218 single ch
Single chain Apo-2
Antibody light cha
Antibody light cha
Antibody light cha
Antibody light cha
Antibody light cha
VL domain CDR of a
Human anti-DAF ant
Amino acid sequenc
Amino acid sequenc

PS Claim 8; Page 16; 21pp; English.

XX

CC The present invention describes a high-affinity monoclonal antibody

CC characterised by an acid-washed enzyme-linked immunosorbent assay (EIA).

CC The antibody is used in cancer therapy. Association of the new antibody

CC with an antigen is favoured over dissociation in vivo and they therefore

CC have longer localisation times at target sites, resulting in a higher

CC concentration of antibodies localised at the target sites. Targeting the

CC antibody to a site in vivo is improved. The concentration of antibody

CC does not need to be too high which reduces side-effects and costs of

CC therapy. The present sequence represents the light chain variable region

CC of a monoclonal antibody having affinity for carcinoembryonic antigen

CC (CEA), a tumour associated antigen), which is used in the exemplification

CC of the present invention.

CC

XX

SO Sequence 111 AA;

QY Query Match 100.0%; Score 564; DB 21; Length 111;

Db Best Local Similarity 100.0%; Pred. No. 2.3e-38;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDVLRPPSSVSGSLQQRVSITCGSSSSNIGNANYGWIQVPGSAPRLILSATTPRAGI 60

Db 1 qdvlrppssvsgslqqrvsitcsgssnignanygwvqvpgsaprllisattdrasgi 60

QY 61 PDREFGSRSGNATATLTISSLQAEDEADYRCASVOSYSGVSGFSGTRLPVVG 111

Db 61 pdrefgsrsgnatatlTISSlqaeadeadyrcasvgsygsfgstrltlvlg 111

RESULT 2

AAM39507

AAAM39507 standard; Protein; 147 AA.

XX AC

XX AAM39507;

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2652.

XX

XX Human polypeptide SEQ ID NO 2652.

KW Human; noctropic; immunosuppressant; cyostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokineic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PF 26-DEC-2000; 2000WO-US34263.

XX

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX

PA (HXSE-) HXSEQ INC.

XX

PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX

WP1: 2001-442253/47.

XX

NR N-PSDB; AAI58663.

```

xx      Novel nucleic acids and polypeptides, useful for treating disorders
pt      such as central nervous system injuries -
ps      Example 4; SEQ ID NO 2652; 10078bp; English.
xx
xx      The invention relates to human nucleic acids (AA157798-AA161369) and
cc      the encoded polypeptides (AA38642-AA42213) with nootropic,
cc      immunosuppressant and cytostatic activity. The polynucleotides are useful
cc      in gene therapy. A composition containing a polypeptide or polynucleotide
cc      of the invention may be used to treat diseases of the peripheral nervous
cc      system, such as peripheral nervous injuries, peripheral neuropathy and
cc      Alzheimer's, Parkinson's disease, central nervous system diseases, such as
cc      lateral sclerosis, and Shy-Drager syndrome. Other uses include the
cc      utilisation of the activities such as: Immune system suppression,
cc      Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
cc      and thrombolytic activity, cancer diagnosis and therapy, drug screening,
cc      assays for receptor activity, arthritis and inflammation, leukaemias and
cc      C.N.S disorders.
cc      Note: The sequence data for this patent did not form part of the printed
cc      specification.
xx
xx      Sequence      147 AA:
xx
xx      Query Match          69.0%; Score 389; DB 22; Length 147;
xx      Best Local Similarity 67.3%; Pred. No. 3.5e-24;
xx      Matches 76; Conservative 16; Mismatches 19; Indels 2; Gaps 1;:
xx
xx      1 QDVLTPSPSSVSGLCORNSITCGSSSSNIGNAVYGMVQOVPGSAPRLILISATTDRAAGI 60
xx      10 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
xx      20 gsvltpqpsvsgdpagqrylvlscitgssnlgdydvhwgqlpgtbpklllygnsnmpsgv 79
xx
xx      61 PRFGSGRSGNATLTILSSLOADEADYVCAYOSQSYGS--VFSGGTRFLTVIG 111
xx      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
xx      80 pdrfgsksgtstaiaiglgadeadyyccgsydsjslsgvvfgyggtklvtlg 132
xx
xx      RESULT      3
xx      AAB36209
xx      ID      AAB36209 standard; protein; 236 AA.
xx
xx      AAB36209:
xx
xx      DT      15-FEB-2001 (first entry)
xx
xx      DE      Human immune system associated protein HISAP-7.
xx
xx      KM      Human; immune system associated protein; HISAP-7; immune disorder;
xx      infection; autoimmune disease; cancer.
xx
xx      OS      Homo sapiens.
xx
xx      PN      US6135941-A.
xx
xx      PD      24-OCT-2000.
xx
xx      PF      27-MAR-1998; 98US-0049672.
xx
xx      PR      27-MAR-1998; 98US-0049672.
xx
xx      PA      (INCY-) INCYTE PHARM INC.
xx
xx      PI      Tang YT, Yue H, Lai P, Corley NC, Guegler KJ, Baughn MR;
xx      Hillman JL, Au-Young J;
xx
xx      WPI: 2001-030926/04.
xx
xx      DR      N-PSDB; AAC66525.
xx
xx      New human immune system associated proteins (HISAP) and polynucleotides
xx      encoding the HISAP, useful for diagnosing, treating or preventing
xx      immune or cell proliferative disorders or infections -

```

XX PS Claim 1: Column 59-62: 54pp; English.

CC The present invention provides the coding and protein sequences for a
XX number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer.

XX Sequence 236 AA:

Query Match 68.9%; Score 388.5; DB 22; Length 236;
Best Local Similarity 67.9%; Pred. No. 6.1e-24;
Matches 76; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 1 QDVLTPSSVSGSLGQRVSTTCSSSSNIGCMAYGVQVPGSAPRLISATTDRAAGI 60
Db 20 qsvltqppsvsgslgqrvsttcscgssnlgagydvmvqqlptglilysrntpsgv 79
QY 61 PDRFSGSRSGNTATLTITSSLAQEDADYCYCASYQSTVSG-VFGSGRTLVLG 111
Db 80 pdrfsgsksgntatltitsslaqeadadycysqstsvsgvifggrtkltvlg 131

RESULT 4
ABG12886
ID ABG12886 standard; Protein; 249 AA.

XX AC ABG12886;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #12877.
XX DE Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YF;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS77073.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
XX PS Claim 20: SEQ ID NO 43245; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 249 AA:

Query Match 68.6%; Score 387; DB 22; Length 249;
Best Local Similarity 65.8%; Pred. No. 8.5e-24;
Matches 73; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

QY 1 QDVLTPSSVSGSLGQRVSTTCSSSSNIGCMAYGVQVPGSAPRLISATTDRAAGI 60
Db 34 qsaltpssasgslgqrvsttcscgtsdignvyvryrhpkpklmlyevtkrpsv 93
QY 61 PDRFSGSRSGNTATLTITSSLAQEDADYCYCASYQSTVSGVFGSGRTLVLG 111
Db 94 pdrfsgsksgntatltitsslaqeadadycysqstsvsgvifggrtkltvlg 144

RESULT 5
AAU02620
ID AAU02620 standard; Protein; 110 AA.

XX AC AAU02620;
XX DT 29-AUG-2001 (first entry)
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 106.
XX DE Antibody: adipocyte; heavy chain; light chain; obesity; fat;
XX KW heart disease; complementarity determining region; CDR.
XX OS Homo sapiens.
XX PN WO200127279-A1.
XX PD 19-APR-2001.
XX PF 11-OCT-2000; 2000WO-GB03900.
XX PR 12-OCT-1999; 99US-0158812.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Edwards BM, Main SH, Vaughan TJ;
XX DR WPI: 2001-282031/29.
XX DR N-PSDB; AAS03520.
XX PT Panel of specific binding members of antibody molecules which bind to
XX PT whole adipocytes is used in the treatment of obesity and obesity
XX PT related diseases -
XX PS Claim 1: Page 167; 182pp; English.

CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC chain, and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody

CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.

Query Match	68.4%	Score 386	DB 22	Length 110
Best Local Similarity	65.5%	Pred. No. 4.6e-24		
Matches 72	Conservative 17	Mismatches 21	Indels 0	Gaps 0

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QY 1 QDVLTPSSSVSGSLGQRYSTCTGSSSSNTGNAVWYQDVGAPRLLISATTDRAAGI 600
   | |||||:|||||:::||||:||||| || |||||:||||| ||:|
DB 1 qsvltqpsavsgspgqstltscftssdvgygyvawyqgqbpqkaplmlyevnkrpsgv 600

```

Qy	61	PDRESGSNGNTATLTITSSIOAEDEADYYCASYOSTYSGVFGSGTRLTVL	110
		: : :	
Db	61	pdrgsgsngntasltvstrlqadeadyyccssyagndsvlffgggckrltlv	110

RESULT	6
AA95205	
ID	AA95205 standard; Protein; 109 AA.

DT	29-AUG-2000	(first entry)
XX		
AC	AAV95205;	
.....		

DE	Anti-platelet glycoprotein Ib human HiB-2 VL.
XX	
KM	Variable light chain: single chain antibody; scFv; human; HiB-2
KM	glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KM	anthrombotic; thrombus; therapy; diagnostic.

OS Homo sapiens.

FH	key	Location/Qualifiers
1	1	1
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4	4	4
5	5	5
6	6	6
7	7	7
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99	99	99
100	100	100

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FT /note= "framework r
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FT /note= "complementarity det

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FT /note= "framework region 2"
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FT /note= "complementarity determining region 2"

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FT /note= "framework region 3"
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FT /note= "complementarity determining region 3"

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FT /note= "framework region 4"
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PN WO200026667-A1

PD 11-MAY-2000.

PF 29-OCT-1999; 99WO-US25495.

PR 30-OCT-1998; 98US-0106275.

PA (MILL/) MILLER J L.

PI Miller JL;

DR WPT; 2000-365744/31.

XX Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
XX inhibit platelet aggregation -
PS Claim 18; Page -; 89pp; English.

Claim 18; Page -; 89pp; English.

CC - The present sequence is that of the light chain variable region
CC (VL) of human single chain antibody (scFv) H1b-2 (see AA195209),
CC which is directed against platelet glycoprotein Ib (GP1b). The H1b
CC series of scFv was isolated from a human synthetic VH and VL scFv
CC library by 3 rounds of phagemid selection against transfected CHO
CC cells expressing the GP1b alpha component of the GP1b/IX/V complex
CC on their surface, followed by a 4th round of selection against
CC washed human platelets, and 2 final rounds in which attempts were
CC made to displace scFv from washed platelets by flooding with
CC murine monoclonal antibody or mimotope peptide (see AA195220).
CC Whether displayed as surface proteins on a phagemid or secreted
CC as free scFv by *Escherichia coli*, the H1b scFv clones are capable
CC of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombi in
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GP1b alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.

CC Note: The present sequence is not shown in the specification but is
CC derived from the H1b-2 VL sequence given in Fig 6 (see AA195220).

SQ Sequence 109 AA;

Query Match	68.4%	Score	385.5	DB	21	Length	109
Best Local Similarity	67.3%	Pred. No.	5e-24				
Match 74, Conservative	16	Mismatches	19			Indels	1
						Gaps	1

```
QY      1 QDVLTPSSVSGSLGQRVSITCGSSSNIGNAYGVWQVPASAPRLILSATPTDRASGI    60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 qsvlqppsaastpgqrvtiscssssnnisn-yvwywqq|psltapklilymmqprsgv    55
```

QY 61 PDRFGSGRGNTATLTLTSSLAQEADEADYYCASYGSTRFSGVFGSGTRLTVL 110
|||||::: :|| || ::|||::|::: : |||| |::|
Db 60 pdrfsgskstaslaiglrseadyycaawddslsgvfgggtkltlv 109

RESULT	7
AAG65569	
ID	AAG65569 standard; protein; 113 AA

AC AAG65569;

DT 30-NOV-2001 (first entry)

DE Amino acid sequence of protein seq Id No. 94.

KW Gene library; immunoglobulin; antibody library; human.

OS Homo sapiens

PN WO200162907-A1

PD 30-AUG-2001.

PF 22-FEB-2001; 2001WO-JP01298.

PR 22-FEB-2000; 2000JP-0050543.

PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.

PI Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;

Query Match	68.3%	Score 385;	DB 22;	Length 113;
Best Local Similarity	67.3%	Pred No. 5.7e-24;		
Matches	76;	Conservative	15;	Mismatches 20;
			Indels	2;
			Gaps	1

RESULT	8
AAG80216	
ID	AAG80216 standard; Protein; 117 AA

KM autoantigen; fusion protein; islet cell antigen; MICA autoantibody;
KM glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;
KM polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;
KM variable region; heavy chain; MICA-6.

PT New fusion protein. Useful for diagnosis of diabetes type I and other

PT glutamate decarboxylase and islet cell antigen

CC This invention describes a novel fusion protein (I) that has, at its
CC N-terminus, one or more epitopes that bind specifically to autoantibodies
CC (Ab) against the islet cell antigen IA2 and, at its C-terminus, one or
CC more epitopes that bind specifically to antibodies (Ab) directed against
CC the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding
CC it, vectors containing (II) and transformed cells, are useful for
CC diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,
CC polyglutathione autoimmune syndrome or other autoimmune conditions
CC associated with Ab against GAD65 or IA2. (I) provides a rapid and simple
CC diagnosis of high specificity and sensitivity, capable of recognizing
CC antibodies against both IA2 and GAD65, simultaneously. Unlike known
CC fusions, where the GAD65 component is at the N-terminus, (I) contains
CC correctly folded conformational epitopes that can react with most MICA
CC autoantibodies. This sequence represents the human autoantibody MICA-6
CC variable region heavy chain used in the method of the invention.

Query Match	68.3%	Score 385;	DB 22;	Length 117;
Best Local Similarity	66.1%	Pred. No. 5.9e-24;		
Matches 72;	Conservative 16;	Mismatches 21;	Indels 0;	Gaps 0

RESULT	9
AAB52208	
ID	AAB52208 standard; Protein; 112 AA

DT 22-FEB-2001 (first entry)

KW Anti-hepatitis B monoclonal antibody; human; hepatitis B; prevention.
KW antiinflammatory; hepatotropic.

PN JP20000253878-A

DR N-PSDB; AAC96953.

Novel anti-hepatitis B monoclonal antibody used for the prevention of

PS Claim 21; Page 18; 27pp; Japanese.

CC This invention relates to a human anti-hepatitis B monoclonal antibody
CC included in the invention are polynucleotide sequences AAC36948 -
CC AAC96955 which encode fragments of the heavy and light chains of the
CC antibody. Proteins and peptides represented by sequences AAB52185 -
CC AAB52210 are fragments of the anti-hepatitis B light and heavy chains.

Db 139 gqvltcpasvsgpqsqstictgtsdgygnyvwyqghpqbapklmlyegsktrpsgv 198
 QY 61 PDRFGSGSRGNATLTLTSSLAQEADEADYCYCAQSTYSGVFGSGTRLTVLG 111
 Db 199 snrtsgsksgnbasltlsglqaeadeaycysstlrstrlvfggkklvlg 249

RESULT 12
 AA058235
 ID AA058235 standard; Protein: 246 AA.
 AC AAY58235;
 DT 27-MAR-2000 (first entry)
 DE Internalising anti-c-erbB-2 receptor antibody scFv F5.
 KW Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;
 OS HER/neu oncogene; tumour-specific; Internalisation; non-Immunogenic.
 XX Synthetic.
 XX Homo sapiens.

Key Location/Qualifiers
 FT 31..35
 FT /note= "Heavy chain variable region (VH) complementarity
 FT determining region 1 (CDR1)"
 FT Region 50..66
 FT /note= "VH-CDR2"
 FT Region 99..108
 FT /note= "VH-CDR3"
 FT Region 157..170
 FT /note= "Light chain variable region (VL) complementarity
 FT determining region 1 (CDR1)"
 FT Region 186..192
 FT /note= "VL-CDR2"
 FT Region 225..235
 FT /note= "VL-CDR3"

MO9955367-A1.
 XX
 XX 04-NOV-1999.
 XX PD
 XX 23-APR-1999; 99WO-US07395.
 XX PF
 XX 24-APR-1998; 98US-0082953.
 XX PR
 XX 12-FEB-1999; 99US-0250056.
 XX PA
 XX (REGC) UNIV CALIFORNIA.
 XX PI
 XX Marks JD, Poul MA;
 XX WPI: 2000-072168/06.
 XX DR N-PSDB; AA058235.
 XX PT Novel internalizing antibodies used to treat cancer cells -
 XX PS Claim 3; Page 81; 85pp; English.

XX This sequence represents an internalising humanised antibody,
 CC scFv F5, which specifically binds to the extracellular domain
 CC of the c-erbB-2 receptor, the protein product of the HER/neu oncogene.
 CC The scFv F5 antibody binds to the epitope of the c-erbB-2 receptor that
 CC is bound by F5 antibodies. On binding the c-erbB-2 receptor, the
 CC antibody is transported into the cell. The c-erbB-2 receptor is a marker
 CC protein which is overexpressed by 30-50% of breast carcinomas and other
 CC adenocarcinomas, and thus provides a useful cell surface marker for
 CC specifically targeting tumour cells. The antibodies of the invention
 CC are used as tumour-targeting molecules for diagnosis and treatment. The
 CC antibodies can be attached to effector molecules. The effector molecules
 CC may include cytotoxins such as ricin, abrin or pseudomonas exotoxin;
 CC radionuclides; ligands such as growth factors; therapeutic agents such

CC as vinblastine, vindesine or melphalan; ribozymes; or antisense
 CC molecules. The antibodies may also be used for in vivo or in vitro
 CC detection and/or quantitation of the c-erbB-2 receptor and thus diagnosis
 CC and/or localisation of cancers characterised by expression of c-erbB-2.
 CC Although antibodies have previously been used to target tumour cells,
 CC their success has been limited. The utility of prior art antibodies has
 CC been hampered by the paucity of tumour specific antibodies, antibody
 CC immunogenicity, low binding affinity, and poor tumour penetration.
 CC Immunogenicity could be avoided and toxicity reduced if high affinity
 CC tumour specific human antibodies were available. However, the production
 CC of human monoclonal antibodies using conventional hybridoma technology
 CC has proven difficult. Also, most of the antibodies produced react with
 CC antigens that are also common to non-malignant cells, which makes them
 CC unsuitable for use as tumour-targeting molecules. The antibodies of the
 CC invention overcome these difficulties, as they are targeted to a
 CC tumour-specific antigen, and avoid the problem of immunogenicity as they
 CC are human in origin.

SQ Sequence 246 AA:
 QY 1 QDVLQPPSSVSGSLGQRVSTTCGSSSNIGNAYVGVQVGGAPRLILSATDRAAGI 60
 Db 135 gqvltcpasvsgpqsqstictgtsdgygnyvwyqghpqbapklmlyegsktrpsgv 194
 QY 61 PDRFGSGSRGNATLTLTSSLAQEADEADYCYCAQSTYSGVFGSGTRLTVLG 111
 Db 199 snrtsgsksgnbasltlsglqaeadeaycgyfysdsglsgwvfggkklvlg 246

RESULT 13
 AA002577
 ID AA002577 standard; Protein: 110 AA.
 AC AA002577;
 DT 29-AUG-2001 (first entry)
 DE Anti-adipocyte monoclonal antibody light chain, FAT 64.
 XX
 XX
 XX 29-AUG-2001 (first entry)
 XX DE
 XX
 XX Anti-body; adipocyte; heavy chain; light chain; obesity; fat;
 XX heart disease; complementarity determining region; CDR.
 XX OS
 XX Homo sapiens.
 XX PN
 XX WO200127279-A1.
 XX PD
 XX 19-APR-2001.
 XX PF
 XX 11-OCT-2000; 2000WO-GB03900.
 XX PR
 XX 12-OCT-1999; 99US-0158812.
 XX PA
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX PI
 XX Edwards BM, Main SH, Vaughan TJ;
 XX WPI: 2001-282031/29.
 XX DR N-PSDB; AA003477.
 XX PT Panel of specific binding members of antibody molecules which bind to
 XX whole adipocytes is used in the treatment of obesity and obesity
 XX related diseases -
 XX PS Claim 1; Page 141; 182pp; English.

XX AA002501-AA002635, and AA002641-AA002748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
 CC chain, and heavy chain complementarity determining regions (CDR) of the

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 12, 2002, 09:22:50 ; Search time 52.21 Seconds

(without alignments)
257.421 Million cell updates/sec

Title: US-09-786-015-2

Perfect score: 614

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	121	21	AAV82528
2	430	70.0	137	14	AAK42796
3	417	67.9	142	22	AAAG6523
4	411.5	67.0	120	20	AAV22432
5	411	66.9	129	14	AAK42798
6	409.5	66.7	137	18	AAW30273
7	406.5	66.2	120	20	AAV22429
8	404.5	65.9	116	17	AAW05823
9	404.5	65.9	120	20	AAV22430
10	404.5	65.9	127	17	AAW05827
11	404.5	65.9	446	17	AAW05829

12	400.5	65.2	120	20	AAV22433
13	393.5	64.1	120	20	AAV22431
14	390.5	63.6	140	18	AAW22538
15	390	63.5	141	14	AAK42797
16	389	63.3	119	21	AAV90818
17	388.5	63.3	120	12	AAK13310
18	388.5	63.3	120	16	AAK77303
19	388.5	63.3	132	15	AAK53331
20	388.5	63.3	132	20	AAV28359
21	387	63.0	120	12	AAK11986
22	385	62.7	119	17	AAK98492
23	384	62.5	138	13	AAK29012
24	384	62.5	138	13	AAK29014
25	384	62.5	256	21	AAV55072
26	384	62.5	260	21	AAV55075
27	384	62.5	367	21	AAV55078
28	384	62.5	381	21	AAV55079
29	384	62.5	519	21	AAV55080
30	384	62.5	546	21	AAV55074
31	384	62.5	626	21	AAV55081
32	384	62.5	640	21	AAV55082
33	383	62.4	119	18	AAW01584
34	382.5	62.3	138	13	AAK21406
35	382	62.2	119	13	AAW42471
36	381	62.1	113	13	AAK21268
37	381	62.1	123	18	AAW07438
38	380	61.9	249	21	AAV69523
39	379.5	61.8	116	22	AAW07513
40	379.5	61.8	239	18	AAW35561
41	379.5	61.8	239	18	AAW09813
42	379.5	61.8	241	13	AAK21261
43	379.5	61.8	241	20	AAV08988
44	379.5	61.8	267	11	AAW04841
45	379.5	61.8	272	13	AAK21260

ALIGNMENTS

RESULT 1	
AAV82528	standard; Protein; 121 AA.
AAV82528:	
AC	AAV82528:
XX	
DT	13-JUL-2000 (first entry)
XX	
DE	Carcinoembryonic antigen affinity antibody heavy chain variable region.
XX	
KW	Carcinoembryonic antigen; CEA; sheep; monoclonal antibody;
KW	tumour associated antigen; anti-carcinogenic; cytostatic;
KW	cancer therapy.
XX	
OS	Ovis sp.
XX	
PN	WO200012556-A1.
XX	
PD	09-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-GB02729.
XX	
PR	28-AUG-1998; 98GB-0018915.
XX	
PA	(KSBI-) KS BIOMEDIX LTD.
XX	
PI	Harrison PJ;
XX	
DR	WPI: 2000-375618/32.
XX	
DR	N-PDSB; AAA08400.
XX	
PT	A new high-affinity monoclonal antibody that is characterized by an
XX	acid-washed enzyme-linked immunosorbent assay for use in cancer therapy

TM27 antibody VH c
TM27 antibody VH c
Murine anti-human
Partial B13/B14 Ab
26OF9 hybridoma VL
HuVh1.3. Syncheli
Variable heavy cha
KM-603 heavy chain
Antibody heavy cha
Human anti-placent
NEM humanised 286
pUC-RVH-PM1f. Syn
pUC-RVH-PM1f-4. S
Interleukin-6 spec
Single chain Fv pr
Single chain Fv pr
Single chain Fv pr
Single chain Fv pr
Single chain Fv pr
Single chain Fv pr
Single chain Fv pr
Lead binding Mab 1
Sequence of the si
NEM humanised hea
Murine VH group 2
Anti-DNA antibody
Anti-CD38 antibody
Antibody gcfv8 hea
EcoRI-HindIII lase
VLys-Linker-VHlys
VH1.3-HuCh1 regio
PUR4125 VL-Lys-syn
Two linked VHlys p
Scrv sequences enc

PS	Claim 8; Page 14; 21np; English.
XX	
CC	The present invention describes a high-affinity monoclonal antibody
CC	characterised by an acid-washed enzyme-linked immunosorbent assay (EIA).
CC	The antibody is used in cancer therapy. Association of the new antibody
CC	with an antigen is favoured over dissociation in vivo and they therefore
CC	have longer localisation times at target sites, resulting in a higher
CC	concentration of antibodies localised at the target sites. Targeting the
CC	antibody to a site in vivo is improved. The concentration of antibody
CC	does not need to be too high which reduces side-effects and costs of
CC	therapy. The present sequence represents the heavy chain variable region
CC	of a monoclonal antibody having affinity for carcinoembryonic antigen
CC	(CEA), a tumour associated antigen), which is used in the exemplification
CC	of the present invention.
XX	
SQ	Sequence 121 AA;
Query Match	100.0%; Score 614; DB 21; Length 121;
Best Local Similarity	100.0%; Pred. No. 3.6e-49;
Matches 121; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 OVQLDESGSLVKKPSQTLTCTVGSGFLTKRYGVSWVRQAPGKALEWIGGVSSGALTAYN 60
Db	1 qvqidesgspvlkvpqqltlctcvsqfsltkkygswvrqapkaletwlgvsssgaltayn 60
OY	61 TALQSRLSVTRDTSKSOPFSLISLSVTTEDTATLYYCAKSYNGDSVPYGLDYWSFGLLITYS 120
Db	61 talqsrllsvtrdtsksqfslislsvtteetatlyycaksvngdsvpdyglwywpjllltys 120
OY	121 S 121
Db	121 s 121
RESULT 2	
ID AAR42796	AAR42796 standard; protein; 137 AA.
XX AC AAR42796;	
XX DT 28-APR-1994 (first entry)	
XX DE Partial B4 Ab variable heavy chain.	
XX KW Monoclonal antibody; mab; light; heavy; chain; variable;	
KM complementarity determining region; CDR; B4; B13/B14; RSV19;	
XX respiratory syncytial virus; RSV; F protein; antigen.	
OS Bos taurus.	
XX FH Key	Location/Qualifiers
FH Region	31..35
FT /label= CDR	
FT Region	50..65
FT /label= CDR	
FT Region	98..118
FT /label= CDR	
FT Misc-difference 3	/note= "residue not defined in the specification"
XX FT	
XX PN WO9320210-A.	
XX PD 14-OCT-1993.	
XX PF 06-APR-1993; 93WO-GB00725.	
XX PR 06-APR-1992; 92GB-0007479.	
XX PA (SCOT-) SCOTGEN LTD.	
XX PI Stott EJ, Taylor G;	
XX	

DR	WPI; 1993-336917/42.
XX	New antibodies against respiratory syncytial virus - including
PT	humanised and chimeric antibodies, useful for treatment,
PT	prevention and diagnosis of infection
XX	
PS	Disclosure; Fig 4; 139pp; English.
XX	
CC	Variable light chain and variable heavy chain sequences derived from
CC	bovine anti-RSV F protein monoclonal antibodies (mAbs) B4 and B13/B14
CC	(AAK42794-R42797), and murine anti-RSV F protein mAb RSV19
CC	(AAQ43376-Q43377), and their CDR peptides, may be used in the design of
CC	fusion proteins (including altered antibodies) which are characterised by
CC	the antigen binding specificity of these mAbs (for humanised Abs, see
CC	AA42798-R42801 and AAR42805-R42808).
CC	NB: the specification is incomplete and published without claims.
XX	
SQ	Sequence 137 AA;
Query Match	70.0%; Score 430; DB 14; Length 137;
Best Local Similarity	67.4%; Pred. No. 3,5e-32;
Matches	87; Conservative 10; Mismatches 24; Indels 8; Gaps 1.
OY	1 QVQLQESGPSTLVKPPSQTLSLTCTVSAGFSLTKYGSMWRQAPGKALEWMIGGVSSGALTAYN 60 : : :
Dd	1 qvxlqesgpslvtkpsqtllstctvsagfsltsysvswvrqapktlewlgaasnggillyn 60
OY	61 TALGSRLSVTRPRTSKSPSLSLSVTTEDTATLYCAKSYNGDSVPYG-----LDVMS 112 : :
Dd	61 palksrlslsvtrprrtksqpslsislvtteptclaclycaksavgdsagsyactgrkgyvdawg 120 : :
OY	113 PGLLTLTVSS 121 :
Dd	121 qglldtvss 129
RESULT 3	
ID	AAG6523 standard; Protein; 142 AA.
XX	AAG6523;
AC	
XX	
XX	22-OCT-2001 (first entry)
DT	
DE	Humanised anti-CTLA4 heavy chain.
XX	
KW	Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
KW	immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
KW	T cell; humanised antibody; autoimmune disorder; graft rejection;
KW	allergy; heavy chain.
XX	
OS	Homo sapiens.
OS	Mus musculus.
OS	Synthetic.
XX	
PN	WO200154732-A1.
XX	
PD	02-AUG-2001.
XX	
PE	26-JAN-2001; 2001WO-USO2653.
XX	
PR	27-JAN-2000; 2000US-0178473.
XX	
PA	(GENY) GENETICS INST INC.
XX	
PI	Careno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
PI	O'Hara D, Hinton P, Tsurushita N;
XX	
DR	WPI; 2001-483195/52.
DR	N-PSTDB; AAH76441; AAH76443.
XX	
PT	Novel antibody-toxic group conjugate comprising an antibody that

Query Match	67.98	Score 417	DB 22	Length 142
Best Local Similarity	66.78	Pred. NO. 5.8e-31		
Matches 82	Conservative 13	Mismatches 26	Indels 2	Gaps 1

OY 1 OVQLQESPSPLVAKFSQSQTLSLCTCYSGSLRYGVSWNRQAAPGKLEMLAGCVSSGLATRN 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 20 qvqlqesgspglivpspqslstlctcvsgfsltsaygywvrppkglewlgyltwagrtlny 79

OY 61 TALDSRLSTRTDTSKSOFSLSSSVTNEPRAIYYCAKSNVGDSVP--YIGDYNSPGLLT 118
| : | | : | : | : | : | | | | | | | | | | : | : | | | | | : | : |
Db 80 salmsrltltskdckngyslklsavtaadcaavycaigpphamkryamdywgqgtlv 139

OY 119 VSS 121
|||
Db 140 vss 142

RESULT 4
AAV22432
ID AAV22432 standard; protein; 120 AA

AC AAY22432;

DT 28-SEP-1999 (first entry)

DE TM27 antibody VH chain mutant V67L, T68S, M69I, L70S, T73N.

KM IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy
 KM autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;
 KM heavy chain.

OS Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
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39	39	39
40	40	40
41	41	41
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63	63	63
64	64	64
65	65	65
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72	72	72
73	73	73
74	74	74
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80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

/Label= V67L

FT /label= T685

FT /label= M69I

FT /label= L70S

FT /label= T73N

PN W09937329-A1.

XX	29-JUL-1999.	
PD		
XX		
PF	15-JAN-1999;	99WO-SE00049.

PR	09-MAR-1998;	98SE-0000766.
PR	22-JAN-1998;	98SE-0000170.

PA (ASTR) ASTRA AB.

PI Flink O, Petren S;

DR WPI; 1999-458611/38.

PT Isotonic pharmaceutical formulations comprising a citrate

PS Claim 12; Page 23-24; 30pp; English

CC This sequence is a mutant of the variable heavy (VH) chain of the
CC antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in
CC the isotonic pharmaceutical formulation of the invention, along with a
CC citrate buffer at a physiologically acceptable pH. The formulations are
CC useful in medical therapy, especially for treatment of autoimmune
CC disease, and particularly, therapy of multiple sclerosis (using the TM27
CC antibody heavy or light chains). The formulation is useful for improving
CC the storage of an antibody. The antibody formulations are simple and
CC effective. The formulations are stable and have improved storage
CC properties. The formulation is simpler than prior art formulations.
CC Existing antibody formulations require the use both of a stabiliser and a
CC buffer. The present invention formulations are stabilised only by citrate
CC buffer in a saline solution at a physiologically preferable pH. The
CC avoidance of low pH prevents undesirable reaction as the site of
CC injection. The formulation does not use ovalbumin for stabilisation,
CC hence avoiding an allergic response to ovalbumin. Also the formulation
CC does not require lyophilisation which is an expensive process and also
CC requires the formulation to be resuspended prior to administration.
XX
XX Sequence 120 AA:
XQ

Query Match	67.08;	Score 411.5;	DB 20;	Length 120;
Best Local	66.18;	Pred. No. 1.5e-30;		
Matches 82;	Conservative 14;	Mismatches 21;	Indels 7;	Gaps 2

QY 1 QVQLQESGPSLVKPSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGCVSSGALTAYN 600

Db 1 qvqlqesgpglvrpsqtlsltctvsgfsltaygvnwvrrppgrglwlgm!wgdgntdyn 60

61 TALQSRSLVTRDTSKSQFSLSLSSVTTEDTAIYYCAKSVNGDSVP---YGLDYWSPGLL 117

Db 61 salksrlskdsknqfslrlssvtaadtavyycar----drvtatl Yamdywgqslv 116

QY 118 TVSS 121

Db 117 tvss 120

RESULT	5
AAR42798	
ID	AAR42798 standard; protein; 129 AA

AC AAR42798;

DT 28-APR-1994 (first entry)

DE B4 HU-VH.

Monoclonal

KW respiratory syncytial virus; RSV; F protein; antigen.

OS Chimeric: Bos taurus.

```

OS Chimeric: Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR
FT Region 50..65
FT /label= CDR
FT Region 98..118
FT /label= CDR
XX
XX WO9320210-A.
XX
XX 14-OCT-1993.
XX
XX 06-APR-1993: 93WO-GB00725.
XX
XX 06-APR-1992: 92GB-0007479.
XX
XX (SCOT-) SCOTGEN LTD.
XX
XX Stott EJ, Taylor G;
XX
XX WPI, 1993-336917/42.
XX
XX New antibodies against respiratory syncytial virus - including
XX humanised and chimeric antibodies, useful for treatment,
XX prevention and diagnosis of infection
XX
XX Disclosure: Fig 10; 139pp; English.
XX
XX Variable light chain and variable heavy chain sequences derived from
XX bovine anti-RSV F protein monoclonal antibodies (mAbs) B4 and B13/B14
XX (AA42794-R42797), and murine anti-RSV F protein mAb RSV19
XX (AA49376-049377), and their CDR peptides, may be used in the design of
XX fusion proteins (including altered antibodies) which are characterised by
XX the antigen binding specificity of these mAbs (for humanised Abs, see
XX CC AA42798-R42801 and AA42805-R42808).
XX NB: the specification is incomplete and published without claims.
XX
XX Sequence 129 AA:
SQ

```

Query Match 66.9%; Score 411; DB 14; Length 129;
 Best Local Similarity 63.6%; Pred. No. 1.8e-30;
 Matches 82; Conservative 13; Mismatches 26; Indels 8; Gaps 1;

```

QY 1 QVQLQESGPSTLVKPSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEMIGVSSGALTAYN 60
   |||||  ||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
Db 1 gvglgsgpglvrpsqglstlctvgfsisysvsvrqpgrglwlgdasnglilyyn 60
QY 61 TALQSLSTVTRDTSKQSFSLSSVTTEPTAIYYCAKSVNGDSVPYG-----LDYWS 112
   ||:||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||
Db 61 palksvtrltldtsknqfslrlssvtaadlavycakscvgsdysgactgrkgydavg 120
QY 113 PGLLTVSS 121
   | :||||
Db 121 ggtltcvss 129

```

RESULT 6
 AAM30273
 ID AAM30273 standard; Protein; 137 AA.
 AC AAM30273;
 XX
 XX 07-JUL-1998 (first entry)
 XX
 XX Heavy chain of HUM4TS.22.
 DE
 XX HUM4TS.22: antibody; platelet derived growth beta receptor; PDGF-R beta;
 KM inhibition; intimal hyperplasia; vasculature; restenosis; angioplasty;
 XX heavy chain.

```

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 58..137
FT /note= "Mature Protein"
FT Binding-site 49..54
FT /note= "Complementarity determining region 1"
FT Binding-site 68..84
FT /note= "Complementarity determining region 2"
FT Binding-site 116..126
FT /note= "Complementarity determining region 3"
FT Misc-difference 20
FT /note= "Optionally Asn at position 1 of mature protein"
FT Misc-difference 49
FT /note= "Optionally Ser at position 30 of the mature protein"
FT Misc-difference 56
FT /note= "Optionally Ser at position 37 of the mature protein"
FT Misc-difference 66
FT /note= "Optionally Ile at position 48 of the mature protein"
FT Misc-difference 86
FT /note= "Optionally Ile at position 67 of the mature protein"
FT Misc-difference 92
FT /note= "Optionally Val at position 73 of the mature protein"
FT Misc-difference 93
FT /note= "Optionally Leu, Ile, and Met at position 74 of the mature protein"
FT Misc-difference 102
FT /note= "Optionally Ile at position 74 of the mature protein"102
XX
XX WO9737029-A1.
XX
XX 09-OCT-1997.
XX
XX 19-MAR-1997: 97WO-US04198.
XX
XX 22-MAR-1996: 96US-0621751.
XX
XX (BOE ) BOEHRINGER MANNHEIM GMBH.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Chang CN, Landolfi NF, Martin U;
XX
XX WPI, 1997-503114/46.
XX
XX N-PSDB: AAT90980.
XX
XX Antibodies to platelet derived growth factor beta receptor - inhibit
XX PDGF BB-induced proliferation of cells expressing the receptor, used
XX particularly for inhibiting intimal hyperplasia
XX
XX Claim 6; Fig 2C; 87pp; English.
XX
XX This is the amino acid sequence for the heavy chain of HUM4TS.22, a
XX novel antibody which specifically binds to the platelet derived
XX growth beta receptor (PDGF-R beta), but not within the fifth
XX extracellular Ig-like domain, where the antibody inhibits PDGF
XX BB-induced proliferation of a cell expressing the PDGF beta receptor.
XX The antibody can be used in a method of inhibiting intimal hyperplasia
XX in the vasculature of a mammal. The antibodies can be used for the
XX treatment of disorders related to PDGF activity such as disorders
XX involving proliferation of smooth muscle cells, and including
XX restenosis following angioplasty.
XX
XX Sequence 137 AA:
SQ

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Query Match 66.7%; Score 409.5; DB 18; Length 137;


```

XX 29-FEB-1996; 96WO-US02754.
PF
XX
XX 01-MAR-1995; 95US-0397411.
PR
XX
XX (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Glingrich R, Link BK, Tso JY, Weiner G;
PI
XX WPI; 1996-412742/41.
DR
XX
XX New bispecific antibody reactive with both T or NK cells and
PT malignant B cells - also their humanised forms and hybridomas
PT producing them, useful for treating or preventing leukaemia,
PT lymphoma and myeloma
XX
XX Claim 14; Fig 4b; 85pp; English.
PS
XX The variable region (AAW05823) of the humanised ID10 antibody heavy
CC chain (AAW05829) consists of human IC4 heavy chain variable region
CC framework (subst. at 9 positions with mouse or consensus human
CC amino acids) and complementarity determining regions from the
CC murine ID10 antibody specific for a 28/32 kDa heterodimeric antigen
CC present on the surface of malignant B-cells. It can be coexpressed
CC with humanised ID10 light chain (see also AAW05828) in e.g. mouse
CC myeloma NSO cells. Humanised antibody fragments can be incorporated
CC into novel bispecific antibodies reactive with both effector cell
CC antigens (see also AAW05824-25, AAW05826 and AAW05830) and malignant
CC B-cells.
XX
XX Sequence 116 AA;
SQ
Query Match 65.9%; Score 404.5; DB 17; Length 116;
Best Local Similarity 64.5%; Pred. No. 6.5e-30;
Matches 78; Conservative 15; Mismatches 23; Indels 5; Gaps 1;
QY 1 QVQLQESGSPSLVLRPQSTLTCTVSGFSLTKYGVSWVRQAPGKALEMVGSSGALTAYN 60
DB 1 QVQLGSGPGLVPRQSTLTCTVSGFSLTKYGVSWVRQAPGKALEMVGSSGALTAYN 60
QY 61 TALQSRISVTRDTSKQSFSLSSVTTEPDATYYCAKSVNGDSVPYGLDWMSFGLLTVS 120
DB 61 aatistltskdtsknqvsliknslcaadtavyycaandr-----yamdywsggtlvtvs 115
QY 121 S 121
DB 116 s 116
RESULT 9
AAW22430
ID AAW22430 standard; protein; 120 AA.
XX
XX AAW22430;
AC
XX 28-SEP-1999 (first entry)
DT
XX TM27 antibody VH chain mutant L48I.
DE
XX
XX Igg antibody; TM27; variable chain; immunoglobulin G; medical therapy;
KW autoimmune disease; multiple sclerosis; antibody storage; VH; muten;
XX heavy chain.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 48
FT /Label= L48I
XX
XX W09937329-A1.

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PD 29-JUL-1999.
XX
XX 15-JAN-1999; 99WO-SE00049.
PF
XX
XX 09-MAR-1998; 98SE-0000766.
PR
XX 22-JAN-1998; 98SE-0000170.
XX
XX (ASTRA) ASTRA AB.
PA
XX
XX Flink O, Petren S;
PI
XX WPI; 1999-458611/38.
DR
XX
XX Isotonic pharmaceutical antibody formulations comprising a citrate
PT buffer, have improved storage
PT
XX
XX Claim 12; Page 20-21; 30pp; English.
PS
XX This sequence is a mutant of the variable heavy (VH) chain of the
CC antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in
CC the isotonic pharmaceutical formulation of the invention, along with a
CC citrate buffer at a physiologically acceptable pH. The formulations are
CC useful in medical therapy, especially for treatment of autoimmune
CC disease, and particularly, therapy of multiple sclerosis (using the TM27
CC antibody heavy or light chains). The formulation is useful for improving
CC the storage of an antibody. The antibody formulations are simple and
CC effective. The formulations are stable and have improved storage
CC properties. The formulation is simpler than prior art formulations.
CC Existing antibody formulations require the use both of a stabiliser and a
CC buffer. The present invention formulations are stabilized only by citrate
CC buffer in a saline solution at a physiologically preferable pH. The
CC avoidance of low pH prevents undesirable reaction as the site of
CC injection. The formulation does not use ovalbumin for stabilisation,
CC hence avoiding an allergic response to ovalbumin. Also the formulation
CC does not require lyophilisation which is an expensive process and also
CC requires the formulation to be resuspended prior to administration.
XX
XX Sequence 120 AA;
SQ
Query Match 65.9%; Score 404.5; DB 20; Length 120;
Best Local Similarity 64.5%; Pred. No. 6.8e-30;
Matches 80; Conservative 16; Mismatches 21; Indels 7; Gaps 2;
QY 1 QVQLQESGSPSLVLRPQSTLTCTVSGFSLTKYGVSWVRQAPGKALEMVGSSGALTAYN 60
DB 1 QVQLGSGPGLVPRQSTLTCTVSGFSLTKYGVSWVRQAPGKALEMVGSSGALTAYN 60
QY 61 TALQSRISVTRDTSKQSFSLSSVTTEPDATYYCAKSVNGDSVPYGLDWMSFGLL 117
DB 61 saltsrvtmldtsknqfsrlrslsvtcaadtavyycaar---drvratlyamdywsggsly 116
QY 118 TVSS 121
DB 117 tvss 120
RESULT 10
AAW05827
ID AAW05827 standard; protein; 273 AA.
XX
XX AAW05827;
AC
XX 27-JAN-1997 (first entry)
DT
XX
XX Humanised ID10 antibody heavy chain.
DE
XX
XX B-cell lymphoma; humanised antibody; bispecific antibody;
KW myeloma; leukaemia; hybridoma; monoclonal antibody.
XX
XX Chimeric Homo sapiens;.
OS
XX Chimeric Mus sp.

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FH Key Location/Qualifiers
FT Domain 1..116
FT /label= Variable_domain
FT Region 31..35
FT /label= CDR1
FT Region 50..65
FT /label= CDR2
FT Region 98..105
FT /label= CDR3
FT Domain 117..214
FT /label= CH1
FT Domain 215..234
FT /label= Hinge
FT Domain 235..273
FT /label= Fos_leucine_zipper
FT Domain 340..446
FT /label= CH3

XX
XX WO9626964-A1.
XX
XX 06-SEP-1996.
XX
XX 29-FEB-1996; 96WO-US02754.
XX
XX 01-MAR-1995; 95US-0397411.
XX
XX (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Glingrich R, Link BK, Tso JY, Weiner G;
XX
XX WPI; 1996-412742/41.
XX
XX New bispecific antibody reactive with both T or NK cells and
XX malignant B cells - also their humanised forms and hybridomas
XX producing them, useful for treating or preventing leukaemia,
XX lymphoma and myeloma
XX
XX Claim 28; Fig 4d; 85pp; English.
XX
XX The humanised ID10 antibody heavy chain (AAW05827) includes a
XX variable region (see also AAW05823) consisting of human R3.5HG heavy
XX chain variable region framework and complementarity determining
XX regions from the murine ID10 antibody specific for a 28/32 kDa
XX antigen found on the surface of malignant B-cells. It can be
XX coexpressed with humanised ID10 light chain (see also AAW05828) in
XX mammalian host cells. Bispecific antibodies can be constructed that
XX include a first binding fragment comprising humanised M291 heavy and
XX light chain variable regions (see also AAW05826, AAW05830), and a second
XX binding fragment comprising humanised ID10 heavy and light chain
XX variable regions. Such antibodies are reactive with both T or NK
XX cells and malignant B cells, and have therapeutic and diagnostic
XX appls.
XX
XX Sequence 273 AA:
SQ

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Query Match 65.9%; Score 404.5; DB 17; Length 273;
Best Local Similarity 64.5%; Pred. No. 1.7e-29;
Matches 78; Conservative 15; Mismatches 23; Indels 5; Gaps 1;

```

```

OY 1 QVOLOEGSPSLVPSQGLSLTCTVSGFSLTKYGVSWRQAPGKALEMLGCVSSGALTAYN 60
DB 1 qyqlqesggj\kpseltlctctvsgfstltnygvhwirvsgpkglwlvkwsqgsteyn 60
OY 61 TALQSRSLSTRTPTSKSQSFLSLSVTTEDPTAIYCAKSVNGDSVPYGLDYWSPGLLTWS 120
DB 61 aafisrltiskdskxngvalkinsltaadctavycarndr-----yamdywsgglvtvs 115
OY 121 S 121
DB 116 S 116

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RESULT 11
AAW05829
ID AAW05829 standard; Protein; 446 AA.
XX
XX AAW05829;
XX
XX 27-JAN-1997 (first entry)
XX
XX Humanised ID10 antibody heavy chain.
XX
XX B-cell lymphoma; humanised antibody; bispecific antibody;
XX myeloma; leukaemia; hybridoma; monoclonal antibody.
XX
XX Chimeric Homo sapiens.
XX Chimeric Mus sp.
XX
XX Key Location/Qualifiers
FT Domain 1..116
FT /label= Variable_domain
FT Region 31..35
FT /label= CDR1
FT Region 50..65
FT /label= CDR2
FT Region 98..105
FT /label= CDR3
FT Domain 117..214
FT /label= CH1
FT Domain 215..229
FT /label= Hinge
FT Domain 230..339
FT /label= CH2
FT Domain 340..446
FT /label= CH3

XX
XX WO9626964-A1.
XX
XX 06-SEP-1996.
XX
XX 29-FEB-1996; 96WO-US02754.
XX
XX 01-MAR-1995; 95US-0397411.
XX
XX (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Glingrich R, Link BK, Tso JY, Weiner G;
XX
XX WPI; 1996-412742/41.
XX
XX New bispecific antibody reactive with both T or NK cells and
XX malignant B cells - also their humanised forms and hybridomas
XX producing them, useful for treating or preventing leukaemia,
XX lymphoma and myeloma
XX
XX Example 4; Fig 4e; 85pp; English.
XX
XX The humanised ID10 antibody heavy chain (AAW05829) includes a
XX variable region (see also AAW05823) consisting of human R3.5HG heavy
XX chain variable region framework and complementarity determining
XX regions from the murine ID10 antibody specific for a 28/32 kDa
XX antigen found on the surface of malignant B-cells. It can be
XX coexpressed with humanised ID10 light chain (see also AAW05828) in
XX mammalian host cells. Bispecific antibodies can be constructed that
XX include a first binding fragment comprising humanised M291 heavy and
XX light chain variable regions (see also AAW05826, AAW05830), and a second
XX binding fragment comprising humanised ID10 heavy and light chain
XX variable regions. Such antibodies are reactive with both T or NK
XX cells and malignant B cells, and have therapeutic and diagnostic
XX appls.
XX
XX Sequence 446 AA:
SQ

```


CC the storage of an antibody. The antibody formulations are simple and
CC effective. The formulations are stable and have improved storage
CC properties. The formulation is simpler than prior art formulations.
CC Existing antibody formulations require the use both of a stabiliser
CC buffer. The present invention formulations are stabilized only by citric
CC buffer in a saline solution at a physiologically preferable pH. The
CC avoidance of low pH prevents undesirable reaction as the site of
CC injection. The formulation does not use ovalbumin for stabilisation,
CC hence avoiding an allergic response to ovalbumin. Also the formulation
CC does not require lyophilisation which is an expensive process and also
CC requires the formulation to be resuspended prior to administration.
XX
XX
XX Sequence 120 AA;

Query Match	64.1%	Score 393.5;	DB 20;	Length 120;
Best Local Similarity	63.7%	Pred. No. 6.9e-29;		
Matches	79;	Conservative	15;	Mismatches 23;
			Indels	7;
			Gaps	2
Qy	1	QVQLQESGSPSLKPKSQTSLTCTVSGFSLTKKGVSMWRQAPKALEMLGCVSGSALTAYN	60	
Db	1	qvdqdespgplvrpqstslstctvsgfsltkaygvsmwrqppprglwlgmivgdndtydn	60	
Qy	61	TALQSRLSVTRDTSKQSPSLSSVTTEDTAIFYCAKSVNGDSVP--YGLDYWSPGLIL	117	
		::: :::		
Db	61	salkrvtcmktdtsknqgflrlssvtlaadtavyycaar----drvatallyamdywggsiv	116	
Qy	118	TVSS	121	
Db	117	TVSS	120	

RESULT 14
AAW22538

ID AAW22538 standard; Protein; 140 AA.

AC AAW22538;

DT 03-NOV-1997 (first entry)

DE Murline anti-human class II monoclonal antibody 44H104 VH chain.

KW Antibody; light chain; variable region; hybridoma cell line 44H104
KW immune response; enhance; stimulate; vaccine; immunodiagnosis;
KW antigen delivery.

OS Mus musculus.

PN WO9640941-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-CA00400.

PR 07-JUN-1995; 95US-0483576.

PA (CONN-) CONNAUGHT LAB LTD.

PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH,

DR WPI; 1997-077271/07.
DR N-PSDB; AAT77852.

DR N-PSDB; AAT77852.

PT Recombinant conjugate antibody mol., modified for delivering an
PT antigen - elicits enhanced immune response without the use of
PT adjuvant to generate antibodies which are useful in vaccines or
PT immuno:diagnosis

PS Example 1; Fig 1B; 64pp; English.

CC Novel recombinant conjugate antibody molecules comprise a monoclonal
CC antibody specific for a surface structure of antigen presenting
CC cells (APC), genetically modified to contain at least one antigen

CC exclusively at one or more preslected sites. The conjugate is capable
CC of delivering the antigen to APC and eliciting an immune response to
CC the antigen. The new conjugates are useful as vaccines and are able
CC to elicit an enhanced immune response without the use of an adjuvant.
CC In a specific example, a conjugate was constructed using the murine
CC anti-human class II monoclonal antibody secreted by hybridoma
CC 44H104. The peptide CLTB36 was chosen as antigen; it consists of
CC a tandemly linked T and B cell epitope derived from HIV MN strain.
CC The 44H104 sequence represents the heavy chain variable region
CC from 144H104 which was used in the preparation of a conjugate with
CC antigen CLTB36.
XX
XX Sequence 140 AA;
SQ

Query Match	Similarity	Score	DB	Length
Best Local	62.0%	Pred. No. 1.6e-28;	140;	
Matches	75; Conservative	17; Mismatches	28; Indels	1; Gaps
Qy	1	QVQLDGGPGSLVKKPSQDTSLTCTVSGFSLTKKGVSVNRQAPKALEMLGCVSGSALTAYN	60	
Db	21	qyqlkespgyglvapsgsistctctvgfstlsygvhvrrppbkgylewlvlaagsglnyn	80	
Qy	61	TALQSRSLVTRDTSKSQFSLSLSTVTEEDTAIYYCAKSVNGDSVPGYLDVWSPGLLTIVS	120	
Db	81	slalmrslstskdnfksqyvlkmsisqtdtdtamyccaray-gdyvnyhamydgqstvtas	139	
Qy	121	S	121	
Db	140	s	140	

RESULT 15

ID AAR42797 standard; protein; 141 AA

AC AAR42797

DT 28-APR-1994 (first entry)

DE Partial B13/B14 Ab variable heavy chain

KM Monoclonal antibody; mAb; light; heavy; chain; variable;
KM complementarily determining region; CDR; B4; B13/B14; RSV19;
KM respiratory syncytial virus; RSV; F protein; antigen.

OS Bos taurus.

FH	key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
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99	99	99
100	100	100

FT /label= CDF

FT	/label = CDF
1	0.0
2	0.2
3	0.4
4	0.6
5	0.8
6	1.0

FT	/label = CDF
1	0.0
2	0.2
3	0.4
4	0.6
5	0.8
6	1.0

FT	/note= "residue not defined in the specification"
FT	/note= "residue not defined in the specification"

FT /note- "residue not defined in the specification"

PN WO9320210-A

PD 14-OCT-1993

PF 06-APR-1993; 93WO-GB00725.

PR 06-APR-1992; 92GB-0007479.

PA (SCOT-) SCOTGEN LTD

PI Stott EJ, Taylor G;

DR WPI; 1993-336917/42.

XX New antibodies against respiratory syncytial virus - including
PT humanised and chimaeric antibodies, useful for treatment,
PT prevention and diagnosis of infection
XX

PS Disclosure; Fig 4; 139pp; English.

XX
CC Variable light chain and variable heavy chain sequences derived from
CC bovine anti-RSV F protein monoclonal antibodies (mAbs) B4 and B13/B14
CC (AAK42794-R42797), and murine anti-RSV F protein mAb RSV19
CC (AAO49376-Q49377), and their CDR peptides, may be used in the design of
CC fusion proteins (including altered antibodies) which are characterised by
CC the antigen binding specificity of these mAbs (for humanised Abs, see
CC AAK42798-R42801 and AAK42805-R42808).
CC NB: the specification is incomplete and published without claims.
XX

SO Sequence 141 AA;

Query Match 63.5%; Score 390; DB 14; Length 141;
Best Local Similarity 63.4%; Pred. No. 1.7e-28;
Matches 85; Conservative 10; Mismatches 25; Indels 14; Gaps 3;

QY 1 QVQLQESGPSELVAPSOITLTCTVSGFSLTKYGVSWVROAPGKALEWLGVSAGALTAYN 60
Db 1 qvxlgsgpslvpkpsqslitcvsgslsdhvnvgwlrqapgkalewlgvylykegdkdn 60
QY 61 TALQSRSLVTRDTSKSQFSLSSVPTEDTAIYYCA-----KSVNGDSVPYGL----- 108
Db 61 palksrslslkdnksqgsislsvttedatlycatlgcyfvegvgydct-yglqhttf 119
QY 109 -DYWSPGLLTVSS 121
Db 120 xdawggllvtvss 133

Search completed: August 12, 2002, 09:25:38
Job time: 168 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 12, 2002, 09:23:26 ; Search time 28.26 Seconds
(without alignments)
377.421 Million cell updates/sec

Title: US-09-786-015-4

Perfect score: 564
Sequence: 1 QDVLTQPSVSGSLGGRVSI.....SYQSTYSGVFSGGTRLTVLG 111

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	399.5	70.8	129	2	Ig lambda chain pr
2	391	69.3	111	1	Ig lambda chain pr
3	387	68.6	111	2	Ig lambda chain V
4	387	68.6	235	2	Ig lambda chain -
5	385	68.3	111	2	Ig lambda chain -
6	385	68.3	111	2	Ig lambda chain V
7	382	67.7	111	1	Ig lambda chain V
8	381	67.6	111	1	Ig lambda chain V
9	381	67.6	129	2	Ig lambda chain pr
10	379.5	67.3	235	2	Ig lambda chain -
11	378	67.0	233	2	Ig lambda chain -
12	377	66.8	216	2	Ig lambda chain V
13	376.5	66.8	112	2	Ig lambda chain V
14	376	66.7	136	2	Ig lambda chain V
15	375.5	66.6	236	2	Ig lambda chain -
16	375	66.5	130	2	Ig lambda chain -
17	374	66.3	111	2	Ig lambda chain pr
18	373.5	66.2	112	2	Ig lambda chain V1
19	373	66.1	109	1	Ig lambda chain V
20	373	66.1	111	2	Ig lambda chain V
21	373	66.1	235	2	Ig lambda chain V
22	372	66.0	111	2	Ig lambda chain pr
23	371.5	65.9	149	2	Ig lambda chain V
24	371	65.8	130	1	Ig lambda chain pr
25	370	65.6	111	1	Ig lambda chain V
26	369	65.4	110	2	Ig lambda chain V
27	369	65.4	111	1	Ig lambda chain V
28	369	65.4	111	2	Ig lambda chain V
29	369	65.4	216	2	Ig lambda chain (B

30	368	65.2	111	2	Ig lambda chain V
31	368	65.2	235	2	Ig lambda chain V
32	367.5	65.2	112	1	Ig lambda chain V
33	367	65.1	111	2	Ig lambda chain V
34	367	65.1	235	2	Ig lambda chain V
35	366	64.9	111	1	Ig lambda chain V
36	364.5	64.6	112	2	Ig lambda chain V
37	364	64.5	131	2	Ig lambda chain pr
38	364	64.5	235	2	Ig lambda chain pr
39	363	64.3	111	1	Ig lambda chain V
40	362.5	64.3	217	2	Ig lambda chain V
41	362.5	64.3	217	2	Ig lambda chain V
42	362	64.2	112	2	Ig lambda chain V
43	361	64.0	234	2	Ig lambda chain V
44	359	63.7	112	2	Ig lambda chain V
45	358	63.5	130	2	Ig lambda chain V

ALIGNMENTS

```
RESULT 1
A30554
Ig lambda chain precursor V region - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: A30554
R:Roley, R.C., Beh, K.J.
J. Immunol. 142, 708-711, 1989
A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A:Reference number: A30554; MUID:89039362
A:Accession: A30554
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-129 <FOL>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMV>

Query Match 70.8%; Score 399.5; DB 2; Length 129;
Best Local Similarity 75.9%; Pred. No. 7.1e-26;
Matches 85; Conservative 8; Mismatches 16; Indels 3; Gaps 3;

OY 1 QDVLTQPSVSGSLGGRVSTTCGSSSNIGCMYVQGVPPGAPRRLISATTDASGI 60
Db 20 QAVLTQPSVSGSLGGRVSTTCGSSDNV-GRVGVGVQDPGSGLRITICDPIRPSGV 78

OY 61 PDRFSSRSRGNTATLTITSSIQADEADYYC-ASYQSTYSGVFSGGTRLTVLG 111
Db 79 PDRFSSRSRGNTATLTITSSIQADEADYYCQLAHDSSYN-LFPGGTRLTVLG 129

RESULT 2
L2HUVL
Ig lambda chain V-II region (V1) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01977
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 352, 859-877, 1971
A:Title: Rule of antibody structure. The primary structure of a monoclonal immunoglob
A:Reference number: A01977; MUID:71215142
A:Accession: A01977
A:Molecule type: protein
A:Residues: 1-111 <PON>
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into
```


[illegible]

```

Query Match          67.3%  Score 379.5;  DB: 2;  Length 235;
Best Local Similarity 65.5%  Pred. No. 5.3e-24;
Matches 74;  Conservative 17;  Mismatches 19;  Indels 3;  Gaps 2;

QY 1 QDVLTPSSVSGSLGQRYVSYICSGSSSSNIGNAVYQVPGSAPRLILSATTDRAAGI 60
      |||||  ||  ||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 19 QSVLTGPSAPSGTGGQRYVILICSGSSSSNIGNT-VNMYQLPGRAPKLLHSNNQRPESGV 77
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 PDRESGSSGNTATLTITSSLOADEADYYCASTYSTSG-VFSGRTPLVIG 111
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 78 PDRESGSSGTSSTSLAISGLSEDEADYYCAMDPLNGRYVFGTGYVLG 130
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 11
S25752
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25752
R:Combratoro, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(Lambda) and J(Lambda)-C(Lambda) gene segments of the human immunoglobulin Jart
A:Reference number: S16439; M01D:91257162
A:Accession: S25752
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57817; NID:933733; PIDN:CAAA0954.1; PID:933734
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
C:148-216/Domain: immunoglobulin homology <IM>

```

Query March	67.0%	Score 378;	DB 2;	Length 233;
Best Local Similarity	66.1%	Pred. No. 7e-24;		
Matches 74;	Conservative 16;	Mismatches 20;	Indels 2;	Gaps 2;
QY	1	QDVLTPSPSVSGSGORVSI	FCSSSSNIGNAVYQVPGSAPRLISATTDRA	SCI 60
DB	18	QSVLPQPSASGTPGQRTV	ISCSGSSNIGSNT-VNMVQQLPGTAPKLLITRN	NOQPSGV 76
QY	61	PDRFSRSGMTATLTISL	QAEADYDCASYSOTYSG-FEGSGTRLTIVG	111
DB	77	PDRFSGKSGTISASLT	ISGLQSEDEADYTCAMDSDLGVVFGGKTJLTIVG	128

```

RESULT      12
S29258
Ig lambda chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence-revision 25-Apr-1997 #text-change 21-Jan-2000
C:Accession: S29258
R:Chouhan, L.; van Spriensen, A.; Breyer, J.; Gugieli, P.; Strosberg, A.D.
Eur. J. Biochem. 207, 1115-1121, 1992
A:Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment
A:Reference number: S29257; MUID:92362614
A:Accession: S29258
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-216 <CHO>
A:Note: only part of the coding sequence is given
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: pyroglutamic acid
F:131-199/Domain: Immunoglobulin homology <IM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

```

[illegible]

```

RESULT 13
S51148
antibody light chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S51148
R:de Kruijf, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A:Description: Selection and application of human SCFV antibody fragments from a semi
A:Reference number: S51147
A:Accession: S51148
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <DEK>
A:Cross-references: EMBL:X83713
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
;13-90/Domain: Immunoglobulin homology <IMM>

```

Query Match	66.8%	Score 376.5	DB 2	Length 112:
Best Local Similarity	67.0%	Pred. No. 4.6e-24		
Matches	73:	Conservative 16:	Mismatches 19:	Indels 1:
			Gaps	1:
QY	4	LTQPSVSGSLGQRFVISCSSNIGGNAVYQWQVPGSAPRLLSATTDRAIGIPDR	63	
		: :	:	::
		: :	:	::
Db	2	LTQPSVSGAPQQRFTISCTGSSNIGAGYDHWQOLGTAPKLLITGNSNRPSGVPR	61	
QY	64	FSGSRGMAATLTISLQAEDEADYYCASYSTYSG-VFSGSTRLLTLC	111	
		: :	:	
Db	62	FSGSRGTSASLITGLQAEDEADYYCQSYDSSLGSAFGGCTKLTLVLG	110	

RESULT 14
S16848
Ig lambda chain V-II region precursor - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
!Accession: S60297; S16848

R:Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.

Immunol. Lett. 34, 57-62, 1992

A:Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm

A:Reference number: S60295; MUID:93122853

A:Accession: S60297

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KU2>

A:Cross-references: EMBL:X62125; NID:g38334; PIDN:CAA44056.1; PID:g38335

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:34-111/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 66.7%; Score 376; DB 2; Length 136;

Matches 69; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

QY 1 QDVLQPPSSVSGSLGQRVITCGSSSSNIGNAYVGYQVPGSAPRLISATTDRAAGI 60

DB 20 QSALQPPSASGSPQSVITSGTCTGTSDDGATNYSWYQHHPKAPKLMAYSEKPSGV 79

QY 61 PDRFGSGRSGNTATLTISLQAEDADYCCASYQSTYSGVFGSGTRLTVLG 111

DB 80 PDRFGSGRSGNTATLTISLQAEDADYCCASYQSTYSGVFGSGTRLTVLG 130

RESULT 15

S25746

Ig lambda chain - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25746

R:Combrato, G.; Klobeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam

A:Reference number: S16439; MUID:91257162

A:Accession: S25746

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Cross-references: EMBL:X57811; NID:g33721; PIDN:CAA40948.1; PID:g33722

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:151-219/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 66.6%; Score 375.5; DB 2; Length 236;

Matches 72; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 QDVLQPPSSVSGSLGQRVITCGSSSSNIGNAYVGYQVPGSAPRLISATTDRAAGI 60

DB 20 QSALQPPSASGSPQSVITSGTCTGTSDDGATNYSWYQHHPKAPKLMAYSEKPSGV 79

QY 61 PDRFGSGRSGNTATLTISLQAEDADYCCASYQSTYSGVFGSGTRLTVLG 111

DB 80 PDRFGSGRSGNTATLTISLQAEDADYCCASYQSTYSGVFGSGTRLTVLG 131

Search completed: August 12, 2002, 09:23:27
Job time: 37 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2002, 09:23:49 ; Search time 15.82 Seconds

(without alignments)
271.673 Million cell updates/sec

Title: US-09-786-015-4

Perfect score: 564
Sequence: 1 QDVLTPSSVSSSLGQRVSI.....SYGSTYSGVGSGTRLTVLG 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	391	69.3	111	1	P01711 homo sapien
2	382	67.7	111	1	P01709 homo sapien
3	381	67.6	111	1	P01706 homo sapien
4	373	66.1	109	1	P01708 homo sapien
5	371	65.8	130	1	P06316 homo sapien
6	370	65.6	111	1	P01707 homo sapien
7	369	65.4	111	1	P01710 homo sapien
8	367.5	65.2	112	1	P04209 homo sapien
9	366	64.9	111	1	P01712 homo sapien
10	363	64.4	111	1	P01702 homo sapien
11	354.5	62.9	112	1	P06887 homo sapien
12	347.5	61.6	112	1	P01700 homo sapien
13	347	61.5	111	1	P01705 homo sapien
14	344	61.0	109	1	P06888 homo sapien
15	342	60.6	111	1	P01699 homo sapien
16	341	60.5	109	1	P04208 homo sapien
17	340	60.3	111	1	P01704 homo sapien
18	332	58.9	111	1	P01701 homo sapien
19	331.5	58.8	110	1	P01713 homo sapien
20	319	56.6	103	1	P01703 homo sapien
21	314	55.7	111	1	P08422 homo sapien
22	311	55.1	106	1	P01715 homo sapien
23	309	54.8	111	1	P06318 homo sapien
24	307.5	54.5	131	1	P06319 homo sapien
25	306.5	54.3	112	1	P01721 homo sapien
26	305	54.1	111	1	P01716 homo sapien
27	305	53.0	111	1	P06889 homo sapien
28	299	53.0	106	1	P01717 homo sapien
29	298	52.8	107	1	P01718 homo sapien
30	294	52.1	108	1	P01714 homo sapien
31	292	51.8	108	1	P08748 homo sapien
32	291	51.6	111	1	P01718 homo sapien
33	280	49.6	106	1	P01718 homo sapien

34	272.5	48.3	114	1	P01625 homo sapien
35	270	47.9	111	1	P01720 homo sapien
36	269.5	47.8	113	1	P04210 gallus galli
37	267.5	47.4	108	1	P01605 homo sapien
38	265.5	47.1	108	1	P01607 homo sapien
39	264.5	46.9	129	1	P04431 homo sapien
40	264	46.8	109	1	P01623 homo sapien
41	264	46.8	129	1	P01680 mus musculus
42	262	46.5	109	1	P01612 homo sapien
43	261.5	46.4	112	1	P01722 homo sapien
44	260	46.1	109	1	P01622 homo sapien
45	259	45.9	133	1	P06313 homo sapien

ALIGNMENTS

RESULT 1					
ID	LV2H_HUMAN	STANDARD;	PRT;	111 AA.	
AC	P01711;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig lambda chain V-II region VIL.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=71215142; PubMed=5087637;				
RA	Ponstingl H., Hilschmann N.;				
RT	"Structural rule of antibodies. Complete primary structure of a				
RT	monoclonal immunoglobulin L chain of the lambda type, subgroup II				
RT	(Bence Jones' protein VIL)."				
RL	Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).				
CC	-1- MISCELLANEOUS; THIS IS A BENCE-JONES PROTEIN.				
DR	PIR: A01977; L2HUVL.				
DR	HSSP; P01709; 2MCG.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
KW	Immunoglobulin V region; Bence-Jones protein.				
FT	DISULFID 22 90				
FT	NON_TER 111				
FT	SEQUENCE 111 AA; 11445 MW; 3913736B3EF367E0 CRC64;				
Query Match	69.3%;	Score 391;	DB 1;	Length 111;	
Best Local Similarity	67.6%;	Pred. No. 6.6e-32;			
Matches 73;	Conservative 19;	Mismatches 16;	Indels 0;	Gaps 0;	
OY	4 LVPPSSVSSSLGQRVSIITSCGSSNIGNAVYGVQVPGSARLLISATTDRAQIPDR 63				
DB	4 LVQPAVSSSLGQITISCTGTSDDVGYVSMFQDHGTAKLLISEVRNRPQGVSDR 63				
OY	64 FGSRSRGNTATLTITSSLAQDEADYVCASYOSTYSGVSGTRLTVLG 111				
DB	64 FGSRSKANTASLTISGLQADEADYCCSYTSNVSVFQGTGRLTVLG 111				
RESULT 2					
ID	LV2F_HUMAN	STANDARD;	PRT;	111 AA.	
AC	P01709;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig lambda chain V-II region MGC.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxId=9606;
RP	SEQUENCE.
RX	MEDLINE=75013804; PubMed=4415202;
RA	Fett J.W., Deutsch H.F.;
RT	"Primary structure of the M α g lambda chain.";
RL	Biochemistry 13:4102-4114(1974).
RN	[2]
RP	LAMBDA CHAIN GENES.
RX	MEDLINE=76093781; PubMed=812801;
RA	Fett J.W., Deutsch H.F.;
RT	"A new lambda-chain gene.";
RL	Immunochimistry 12:643-652(1975).
RN	[3]
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA	Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RT	Panagiotopoulos N.;
RL	"Notional allomerism and divergent evolution of domains in
RT	immunoglobulin light chains.";
RL	Biochemistry 14:3953-3961(1975).
RN	[4]
RP	X-RAY CRYSTALLOGRAPHY.
RX	MEDLINE=90133913; PubMed=2515285;
RA	Ely K.R., Herion J.N., Harker M., Edmundson A.B.;
RT	"Three-dimensional structure of a light chain dimer crystallized in
RT	water. Conformational flexibility of a molecule in two crystal
RT	forms.";
RL	J. Mol. Biol. 210:601-615(1989).
CC	-1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
CC	-1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
CC	A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
CC	SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC	MARKERS.
DR	PIR; A01975; L2H0MC.
DR	PDB; 2MCG; 15-JUL-92.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
KW	SMART; SM00406; IGV; 1.
KW	Immunoglobulin V region; Bence-Jones protein; 3d-structure.
FT	MOD_RBS 1 1
FT	DISULFID 22 90
FT	STRAND 5 5
FT	STRAND 10 12
FT	STRAND 18 23
FT	TURN 26 32
FT	STRAND 36 40
FT	TURN 42 43
FT	STRAND 50 51
FT	TURN 52 54
FT	STRAND 55 55
FT	TURN 62 63
FT	STRAND 66 68
FT	STRAND 72 77
FT	STRAND 82 84
FT	HELIX 86 93
FT	STRAND 99 101
FT	STRAND 105 109
FT	NON_TER 111 111
QO	SEQUENCE 111 AA; 11558 MW; 7C1D6E2FA3377BA CRC64;

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Query March 67.7%; Score 382; DB 1; Length 111;
Best Local Similarity 63.1%; Pred. No. 5 le-31;
Matches 70; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

QY 1 QDVLTPSSVSGSLGQRYSITGSSSSNNGCANYYGWIQVQVGSAPRLLSATTTDRAST 60
  1 1111111111111111111111111111111111111111111111111111111111
Db 1 QSALTQPPSAGSSGLQSVYITSTCTGSSDDGNGYVSWIQVHAQKAPKPVITVEYENKRPSGV 60
  1 PDRFGSRSGMNTATLLTSLQAEADYVYCAQSYOSTYSGVFGSGTGLTVLG 111
  Y

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RESULT	3	
LV2C_HUMAN	STANDARD;	PRT; 111 AA.
AC	P01706;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	Ig lambda chain V-II region BOH.	
OS	Osmo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_Taxid=9606;	
RN	[1]	
RE	SEQUENCE.	
RX	MEDLINE=75115478; PubMed=804002;	
RA	Kohler H., Rudofsky S., Kluszens L.;	
RT	"The primary structure of a human lambda II chain.";	
RL	J. Immunol. 114:415-421(1975).	
CC	-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE O2+ MARKER.	
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN	
PR	PIR: A01972; L2H9BH.	
DR	HSSP; P01709; 2MCG.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	InterPro: IPR003596; Ig_V.	
DR	Pfam: PFO0047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
FT	Immunoglobulin V region.	
KW	MOD_RES	1
FT	DISULFID	22
FT	NON_TER	111
FT	SEQUENCE	111 AA; 11650 MW; 94520309932623E8 CRC64;
		BY SIMILARITY.

```

Query Match      67.6% Score 381 DB 1 Length 111
Best Local Similarity 64.9% Pred. No. 6.4e-31
Matches 72 Conservative 14 Mismatches 25 Indels 0 Gaps 0

QY   1 QDVLTPSPSSVSGSLGQRYSITCSGSSNIGNAVGYWQQVPGSAPRLLIATDTDRASGI 60
     | ||||| ||||| ||||| :||||:||||| ||:||| |||||
Db    1 QSALTLPSPSSVSGSPQSQTVCISAGTSSPDVGSHFESWYQHGPBKAKPLIIVGVNKRPSCGV 60

QY   61 PDRFGSGSSGMATRTITTSILOADEADYYCASYQSTSYSGVSGSGLRYLVLG 111
     | |||||:|||||:||||| ||||| ||||| ::||| || |||||
Db    61 PYRSGSKSSGNMTASTLTISGLQAEDEAHYCCSYAGFTWFVEGGGTNLTVLG 111

RESULT 4
LV2E_HUMAN
ID LV2E_HUMAN STANDARD; PRI: 109 AA.
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
   [1]
RN RP
RP SEQUENCE.
RX MEDLINE=80006606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human Iga1 immunoglobulin. V. Amino acid
   sequence of a human Iga lambda light chain (Bur).";
RL J. Biol. Chem. 254:9006-9016(1979).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
   MARKERS.
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR: A01974; L2H0BR.
```

DR HSSP; P01709; 2MCG.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KW Immunoglobulin V region.
 FT MOD_RES 1
 FT DISULFID 22 90
 FT SITE 91 91
 FT NON_TER 109 109
 FT SEQUENCE 109 AA; 11506 MW; BFD8AE1C5D267FAB CRC64;

Query Match 66.1%; Score 373; DB 1; Length 109;
 Best Local Similarity 64.9%; Pred. No. 3.8e-30;
 Matches 72; Conservative 14; Mismatches 23; Indels 2; Gaps 1;

OY 1 QDVLTPSSVSGSLGQRVSTICGSSSSNIGNAYGVQVPGSAPRLISATTDRAAGI 60
 1 QSALTPPSVSGSPGSHVSTICGTSNVDKYKYSWQGHGKAPKLIYEVSRRPGV 60
 OY 61 PDRESGSRGNATLTISSLOADEADYCCASYQSYSGVSGTRLVLG 111
 61 PDRESGSRGNATLTISSLOADEADYCCASYQSYSGVSGTRLVLG 109

RESULT 5
 LV2G_HUMAN STANDARD; PRT; 130 AA.

AC P06316;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-I region BL2 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85062823; PubMed=6095199;
 RA Tsujimoto Y., Croce C.M.;
 RT "Molecular cloning of a human immunoglobulin lambda chain variable
 RT sequence";
 RL Nucleic Acids Res. 12:8407-8414(1984).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC EMBL; X01147; CA25598.1; -
 DR PIR: A01966; LIHUBL.
 DR HSSP: P01703; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT CHAIN 20 130
 FT DOMAIN 20 115
 FT DOMAIN 116 130
 FT DISULFID 41 108
 FT NON_TER 130 130
 FT SEQUENCE 130 AA; 13564 MW; F444BB17D3A55EBF CRC64;

Query Match 65.8%; Score 371; DB 1; Length 130;

Best Local Similarity 67.0%; Pred. No. 7.3e-30;
 Matches 75; Conservative 14; Mismatches 21; Indels 2; Gaps 2;
 OY 1 QDVLTPSSVSGSLGQRVSTICGSSSSNIGNAYGVQVPGSAPRLISATTDRAAGI 60
 1 QSALTPPSVSGSPGSHVSTICGTSNVDKYKYSWQGHGKAPKLIYEVSRRPGI 78
 OY 61 PDRESGSRGNATLTISSLOADEADYCCASYQSYSG-VFSGTRLVLG 111
 79 PDRESGSRGNATLTISSLOADEADYCCASYQSYSGVSGTRLVLG 130

RESULT 6
 LV2D_HUMAN STANDARD; PRT; 111 AA.

AC P01707;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-II region TRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80114123; PubMed=118915;
 RA Scholz R., Yang C., Hilschmann N.;
 RT "Rule of antibody structure. Primary structure of a human monoclonal
 RT IgM-immunoglobulin (myeloma protein TRO). VI. Amino acid sequence of
 RT the L-chain, lambda-type, subgroup II.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:1903-1918(1979).
 CC -1 MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR: A01973; L2HUTR.
 DR HSSP: P01709; 2MCG.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KW Immunoglobulin V region.
 FT MOD_RES 1
 FT DISULFID 22 90
 FT NON_TER 111 111
 FT SEQUENCE 111 AA; 11561 MW; 99DC457A12E8F6E1 CRC64;

Query Match 65.6%; Score 370; DB 1; Length 111;
 Best Local Similarity 63.1%; Pred. No. 7.7e-30;
 Matches 70; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

OY 1 QDVLTPSSVSGSLGQRVSTICGSSSSNIGNAYGVQVPGSAPRLISATTDRAAGI 60
 1 QSALTPPSVSGSPGSHVSTICGTSNVDKYKYSWQGHGKAPKLIYEVSRRPGV 60
 OY 61 PDRESGSRGNATLTISSLOADEADYCCASYQSYSGVSGTRLVLG 111
 61 PDRESGSRGNATLTISSLOADEADYCCASYQSYSGVSGTRLVLG 111

RESULT 7
 LV2G_HUMAN STANDARD; PRT; 111 AA.

AC P01710;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-II region BO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=71103825; PubMed=55322228;
 RA Wikler M., Putnam F.W.;
 RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
 RT chymotryptic peptides, and sequence of protein Bo.";
 RL J. Biol. Chem. 245:4488-4507(1970).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC PIR: A01976; L2HUBO.
 DR HSSP: P01709; 2MCG.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT MOD_RES 1
 FT DISULFID 1
 FT NON_TER 111
 FT SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 65.4%; Score 369; DB 1; Length 111;
 Best Local Similarity 62.7%; Pred. No. 9.6e-30;
 Matches 69; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

OY 1 QDVLTPSSVSGSLGQVITSCGSSSNIGNAYGVQVGSAPRLIISATTDASGI 60
 DB 1 QSALTQPPASVSGPGSVITISCTGTSVDGNKYVSWYQHPGRAPKLVFEVSGRPSGV 60
 OY 61 PDRFGSRSGNTATLTITSSLQAEDEADYCCASYOSTYSGVSGTRLTIVL 110
 DB 61 PDRFGSRSGNTATLTITSSLQAEDEADYCCASYOSTYSGVSGTRLTIVL 110

RESULT 8
 LV2K_HUMAN STANDARD; PRT; 112 AA.
 AC P04209;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-II region NIG-84.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=85204383; PubMed=3922791;
 RA Tonioke H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
 RT "Amino acid sequence of an amyloidogenic Bence Jones protein in
 RT myeloma-associated systemic amyloidosis.";
 RL FEBS Lett. 185:139-141(1985).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
 CC INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
 CC PIR: A01971; L2HUNG.
 DR HSSP: P01709; 2MCG.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KM Immunoglobulin V region; Amyloid; Bence-Jones protein.
 FT DISULFID 22
 FT NON_TER 112
 FT SEQUENCE 112 AA; 11581 MW; 988FEF363AE1E4F3 CRC64;

Query Match 65.2%; Score 367.5; DB 1; Length 112;
 Best Local Similarity 63.4%; Pred. No. 1.4e-29;
 Matches 71; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

OY 1 QDVLTPSSVSGSLGQVITSCGSSSNIGNAYGVQVGSAPRLIISATTDASGI 60
 DB 1 QSALTQPPASVSGPGSVITISCTGTSVDGNKYVSWYQHPGRAPKLVFEVSGRPSGI 60

OY 61 PDRFGSRSGNTATLTITSSLQAEDEADYCCASYOSTYSGVSGTRLTIVL 111
 DB 61 SNRFGSRSGNTATLTITSSLQAEDEADYCCSFTTNSRAVGGGKRLSVLG 112

RESULT 9
 LV2L_HUMAN STANDARD; PRT; 111 AA.
 AC P01712;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-II region WIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=79062503; PubMed=102365;
 RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
 RT "Amino acid sequence of the human myeloma lambda chain Win.";
 RL Biochim. Biophys. Acta 537:9-21(1978).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC PIR: A01978; L2HOWN.
 DR HSSP: P01709; 2MCG.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT MOD_RES 1
 FT DISULFID 22
 FT NON_TER 111
 FT SEQUENCE 111 AA; 11694 MW; 8C3CEB5FE721B87C CRC64;

Query Match 64.9%; Score 366; DB 1; Length 111;
 Best Local Similarity 63.1%; Pred. No. 1.9e-29;
 Matches 70; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

OY 1 QDVLTPSSVSGSLGQVITSCGSSSNIGNAYGVQVGSAPRLIISATTDASGI 60
 DB 1 QSALTQPPRVSGPGSVITISCTGTSVNTGNHYSWYQDPKVKLVTDYDKRPSGV 60
 OY 61 PDRFGSRSGNTATLTITSSLQAEDEADYCCASYOSTYSGVSGTRLTIVL 111
 DB 61 PDRFGSRSGNTATLTITSSLQAEDEADYCCSISGTYSLIFGGGKRLTVLG 111

RESULT 10
 LV1D_HUMAN STANDARD; PRT; 111 AA.
 AC P01702;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-I region NIG-64.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=83186114; PubMed=6404900;
 RA Kametani F., Takeyasu T., Suzuki S., Shinoda T., Okuyama T.,
 RA Shimizu A.;
 RT "Comparative studies on the structure of the light chains of human
 RT immunoglobulins. IV. Assignment of a subgroup.";
 RL J. Biochem. 93:421-429(1983).
 DR PIR: A01965; L1HUNG.
 DR HSSP: P01703; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.

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DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN
 DE VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 OX 11
 RN RP
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.B., Shikman A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyreactive monoclonal antibodies from
 RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-mysin
 RT antibody V region genes.";
 RL J. Immunol. 161:2020-2031(1998).
 DR EMBL: U96394; AAB66783.1; -.
 FT NON_TPR 1
 SQ SEQUENCE 108 AA; 11594 MW; F4B5DC47BA043F48 CRC64;

Query Match	Similarity	59.8%	Score 337.5	DB 4	length 108
Best Local	Similarity	59.8% <td>Score 337.5 <td>DB 4 <td>length 108</td> </td></td>	Score 337.5 <td>DB 4 <td>length 108</td> </td>	DB 4 <td>length 108</td>	length 108
Matches	65	Conservative	14	Mismatches	12
				Indels	1
				Gaps	1
OY	1	ODVLPQPSAVSSLSGLQRYITSCGSSSSNNGVANYGVQVQVGSAPRLISATTPASGI	60		
Db	1	QSVLPQPSASSTPCQORTITSCGSSSSNNGSN-YIYVQQLQGLTAPKLTILIRNQPSCV	59		
OY	61	PDRESGSRSGNTATLTITSLQAEADADYICASYOSTYSG	99		
Db	60	PDREFGSKSGTASIALISGLRESDADADYICAMDMRLSG	98		

Q96JD2	3	Q96JD2	PRELIMINARY;	PRT;	112 AA.
ID	Q96JD2				
AC	Q96JD2;				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
DE	AMYL10D LAMBDA 6 LIGHT CHAIN VARIABLE REGION NEG (FRAGMENT).				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BONE MARROW;				
RA	Pamietti V., Casarini S., Collì Vignarelli M., Merlini G.,				
RT	"Amyloid lambda 6 light chain variable region NEG.;"				
RL	Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; AF267873; AKS58585.1; -.				
FT	NON_TER	1			
FT	NON_TER	112	112		
SQ	SEQUENCE	112 AA;	11908 MW;	080B4B37E2360B06	CRC64;

Query Match	57.1%;	Score 322;	DB 4;	Length 112;
Best Local Similarity	60.4%;	Pred. No. 5.3e-25;		
Matches	67;	Conservative	14;	Mismatches 26; Indels 4; Gaps 3
QY	3	VLTOPSSVSGSLGQRVSTJCSGSSSSNIGGNAYGVYQOVPGSAPRLILSATTDRAAGIPD	62	
		: : : : : : : :		
Db	3	MLTQGHVSVSGSGKRTITTSCTGSSSRILSNS - VQWYQQRPGSAPNIVMENNORPSGVDP	61	
QY	63	RPSGS - RSGNTATLTITSSLQAEADADYYCASY - GSTYSGVFGSGGTRLTVL	110	
		: : : :		
Db	62	RFSGGIDSSSSNSASLTISGLMTEDEADYYCQGSFDDSTNGVHGGRRLTVL	112	
RESULT	4			
996JDI				

ID	Q96JDI	PRELIMINARY;	PRT;	112 AA.
AC	Q96JDI.			
DT	01-DEC-2001 (TRENBLREL. 19, Created)			
DT	01-DEC-2001 (TRENBLREL. 19, Last sequence update)			
DT	01-DEC-2001 (TRENBLREL. 19, Last annotation update)			
DE	AMYL0ID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).			
OS	Os sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxId:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BONE MARROW;			
RA	Pefetti V., Casarini S., Colli Vignarelli M., Merlini G.;			
RT	"Amyloid lambda 6 light chain variable region PIP."			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF267874; AAK58586.1; -.			
FT	NON_TER	1	1	
FT	NON_TER	112	112	
SO	SEQUENCE	112 AA;	12047 MW;	OD3885AC23567B9F CRC64;

55.4%; Score 312.5; DB 4; Length 112;
 Best Local Similarity 58.6%; Pred. 4.8e-24;
 Matches 65; Conservative 14; Mismatches 29; Indels 3; Gaps 2;

```

QY 3 VLTQPSVSGSLGQVAVITCGSSGSSNIGNNVYGVQVPGCAPRLLSATIDRASGPD 62
    ||| ||| ||| : : : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 MLTQPHSVSESPGKTIITISCTRSSGSLSN-YVQVYQRPASAPITTYIEDNQRRSGVPD 61
    ||| ||| ||| : : : : : ||| : : ||| ||| ||| ||| ||| ||| ||| |||
QY 63 RPSGS--RSGNATLTITSLDAQEDADYVYCASVQSYGVGQSGRLTVLG 111
    ||| ||| ||| : : : : : ||| : : ||| ||| ||| ||| ||| ||| ||| |||
Db 62 RPSGIDSSNSASLTITGLTDEADYVYCASVQSYNNYALFEGGGQTLTVLG 112
    ||| ||| ||| : : : : : ||| : : ||| ||| ||| ||| ||| ||| ||| |||
  
```

RESULT	5		
096JDO			
ID	096JDO	PRELIMINARY;	PRT; 116 AA.
AC	096JDO;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	AWYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BONE MARROW;		
RA	Perfetti V., Casarini S., Colli Vignarelli M., Merlino G.;		
RT	"Amyloid lambda 6 light chain variable region SAR.";		
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.		
RZ	EMBL: AF267875; AAK58587.1; -.		
FT	NON_TER	1	1
FT	NON_TER	116	116
SQ	SEQUENCE	116 AA;	12294 MW; F7B09FA9FAE369E CRC64;

Query Match	55.0%	Score 310;	DB 4;	Length 116;
Best Local Similarity	59.8%	Pred. No. 8,9e-24;		
Matches 67;	Conservative 13;	Mismatches 28;	Indels 4;	Gaps 3;
QY	3	VLPDPSSVSGSLGQRYVSTCGSSSSNICGNAYVGVYQVPGSAPRLISATFDRASGIPD	62	
		: : : : : : : :		
Db	3	MLTPHPHVSSEEPGKGTITTCGSSGSIAFTN-VYVMYQLRPSAPPTVYEDNQRPSSGVPD	61	
QY	63	RFSGS--RSGNTATLTITSLQAEDEADYVCASYOSTSGV-FGSGRTLTIVG	111	
		: : : : : : :		
Db	62	RFGSIBSSNSASALITISGLKTEDEADYICQSYDSSISNTVIFGGSTKLTVLG	113	
RESULT	6			

```
Q9NSD6
ID Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOCYTE;
RA Hohmann A.;
RT "Autoimmunity";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; L43092; AAA69746.2; -.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 53.9%; Score 304; DB 4; Length 107;
Best Local Similarity 60.6%; Pred. No. 3.2e-23;
Matches 66; Conservative 9; Mismatches 30; Indels 4; Gaps 2;

QY 4 LTQPPSSVSGSLGQRVSTICGSSSSNIGNAYVGYQVPGSAPRLISATTDRAAGIPDR 63
DB 2 LTQDPVYVALGQTVIRITQGSLSR---SYASHTYQKQKQAPLVLYIKNNPSPGIPDR 58
QY 64 FGSRSRGNTATLTISLQAEDEADYCCASYQSTYS-GVFGSGTRLTVLG 111
DB 59 FGSSSSGNTASLTITGAQAEDEADYCNRSRDSGNHAFVGGGTRKLVLG 107

RESULT 7
Q9UL82 PRELIMINARY; PRT; 107 AA.
AC Q9UL82:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9827139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035032; AAD56268.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 107
SQ SEQUENCE 107 AA; 11445 MW; 52F0CC1AB26821DC CRC64;
```

```
Query Match 53.5%; Score 301.5; DB 4; Length 107;
Best Local Similarity 59.8%; Pred. No. 5.7e-23;
Matches 64; Conservative 7; Mismatches 33; Indels 3; Gaps 1;

QY 4 LTQPPSSVSGSLGQRVSTICGSSSSNIGNAYVGYQVPGSAPRLISATTDRAAGIPDR 63
DB 4 LTQDPVYVALGQTVIRITQGSLSR---SYASHTYQKQKQAPLVLYIKNNPSPGIPDR 58
QY 64 FGSRSRGNTATLTISLQAEDEADYCCASYQSTYS-GVFGSGTRLTVLG 110
DB 61 FGSSSSGTTLTISLQAEDEADYCCASYQSTYS-GVFGSGTRLTVL 107

RESULT 8
Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 25.4 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003600; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGCL; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 50.0%; Score 282; DB 11; Length 235;
Best Local Similarity 56.2%; Pred. No. 1.4e-20;
Matches 63; Conservative 12; Mismatches 33; Indels 4; Gaps 3;

QY 1 QDVLTOPSSVSGSLGQRVSTICGSSSSNIGNAYVGYQVPGSAPRLISATTDRAAGI 60
DB 20 QLVLTQPPSSVSTSLGSAKLPCKASTGNT-GDSTVNMVQOYMGKSPYNNMIVGGDLRPSGV 78
QY 61 PDFFSGS--RSGNTATLTISLQAEDEADYCCASYQSTYS-GVFGSGTRLTVL 110
DB 79 SDRFSGSDISSNSAFLLITGNQAEDEADYCCASYSGIR-VFGGGTRKLVYL 129

RESULT 9
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
```


Search completed: August 12, 2002, 09:24:41
Job time: 111 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 12, 2002, 09:22:50 ; Search time 28.26 Seconds
(without alignments)
411.423 Million cell updates/sec

Title: US-09-786-015-2

Perfect score: 614

Sequence: 1 OVQOESGSPSLVKSQTLSTL.....DSVPYGLDYMSPGLLTVSS 121

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 28138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450.5	73.4	143	2	SS4249 Ig mu heavy chain
2	444.5	72.4	141	2	SS4236 Ig mu heavy chain
3	443.5	72.2	137	2	SS4234 Ig mu heavy chain
4	442	72.0	140	2	SS4245 Ig mu heavy chain
5	441	71.8	132	2	SS4235 Ig mu heavy chain
6	440	71.7	140	2	SS4239 Ig mu heavy chain
7	439	71.5	140	2	SS4240 Ig mu heavy chain
8	439	71.5	140	2	SS4248 Ig mu heavy chain
9	438.5	71.4	139	2	SS4233 Ig mu heavy chain
10	438	71.3	140	2	SS4242 Ig mu heavy chain
11	436.5	71.1	141	2	SS4226 Ig mu heavy chain
12	436	71.0	142	2	SS4241 Ig mu heavy chain
13	435	70.8	138	2	SS4246 Ig mu heavy chain
14	434.5	70.8	139	2	SS4231 Ig mu heavy chain
15	432	70.4	144	2	SS4244 Ig mu heavy chain
16	431	70.2	140	2	SS4227 Ig mu heavy chain
17	430.5	70.1	140	2	SS2080 Ig mu heavy chain
18	429	69.9	144	2	SS4228 Ig mu heavy chain
19	423	68.9	138	2	SS4225 Ig mu heavy chain
20	420	68.4	142	2	SS4243 Ig mu heavy chain
21	419.5	68.3	141	2	SS4238 Ig mu heavy chain
22	418.5	68.2	139	2	SS4229 Ig mu heavy chain
23	415.5	67.7	145	2	SS4237 Ig mu heavy chain
24	409.5	66.7	145	2	SS4230 Ig mu heavy chain
25	408.5	66.5	139	2	SS4247 Ig mu heavy chain
26	396.5	64.6	592	2	SS2705 Ig mu chain - shee
27	388.5	63.3	472	2	SS1459 Ig gamma-1 chain -
28	383	62.4	142	2	SS4232 Ig mu heavy chain
29	381.5	62.1	122	2	A49049 Ig heavy chain V r

30	380.5	62.0	141	2	SS2446 Ig heavy chain V r
31	378.5	61.6	118	2	SS3286 Ig heavy chain (an
32	375.5	61.2	117	2	S38563 Ig heavy chain V r
33	375.5	61.2	135	2	S31913 Ig gamma-2a chain
34	375	61.1	121	2	D30560 Ig heavy chain V r
35	375	61.1	121	2	S33131 Ig heavy chain V r
36	373.5	60.8	122	2	S20809 Ig heavy chain V r
37	373	60.7	140	2	S14238 Ig gamma-1 chain p
38	373	60.7	140	2	I37782 Ig variable region
39	372.5	60.7	116	2	S42484 Ig heavy chain V r
40	371	60.4	231	2	PC4155 Ig gamma-2b chain
41	370.5	60.3	135	2	PL0100 Ig heavy chain pre
42	370.5	60.3	139	2	A32456 Ig heavy chain pre
43	370	60.3	140	2	SS5028 Ig heavy chain V r
44	369.5	60.2	120	2	PL0087 Ig heavy chain V r
45	369	60.1	117	2	I28195 Ig heavy chain V r

ALIGNMENTS

RESULT 1
SS4249
Ig mu heavy chain V region precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: SS4249
R:Dufoir, V.; Nau, F.
submitted to the EMBL Data Library, April 1995
A:Description: Sheep Immunoglobulin mu heavy chain variable region sequence.
A:Reference number: SS4225
A:Accession: SS4249
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-143 <DUF>
A:Cross-references: EMBL:249193; NID:g794139; PIDN:CNA89052.1; PID:g794140
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:34-116/Domain: Immunoglobulin homology <IMM>

Query Match 73.4%; Score 450.5; DB 2; Length 143;
Best Local Similarity 73.4%; Pred. No. 5.7e-32;
Matches 91; Conservative 11; Mismatches 19; Indels 3; Gaps 1;
QY 1 OVQOESGSPSLVKSQTLSTLTCVSGFSLTKYVSVNRQAPKALMELGCVSSGALTAYN 60
II:|||||
DB 20 QVRLQESGSPSLVKSQTLSTLTCVSGFSLTVNAVGVWVROAPKVPMLGISTDGSSTSYN 79
QY 61 TALQSLVTRDTSKQSVLSSTVTEPTAIYYCAK---SYNGDSVPYGLDYMSPGLL 117
II:|||||
DB 80 PALKSLSTRDTSKQSVLSSTVTEPTAIYYCAKRTFGGGFAVGNDIDWGFLLV 139
QY 118 TVSS 121
DB 140 TVSS 143
RESULT 2
SS4236
Ig mu heavy chain V region precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: SS4236
R:Dufoir, V.; Nau, F.
submitted to the EMBL Data Library, April 1995
A:Description: Sheep Immunoglobulin mu heavy chain variable region sequence.
A:Reference number: SS4225
A:Accession: SS4236
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <DUF>
A:Cross-references: EMBL:249161; NID:g794111; PIDN:CNA89030.1; PID:g794112

A;Accession: S54242

A:Reference number: S54225

A:Accession: S54231

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-139 <DUF>

A:Cross-References: EMBL:Z49167; NID:g794101; PIDN:CAA89036.1; PID:g794102

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: Immunoglobulin

F:34-116/Domain: Immunoglobulin homology <IMM>

Query Match

70.8%; Score 434.5; DB 2; Length 139;

Best Local Similarity 69.4%; Pred. No. 1.3e-30;

Matches 84; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 1 QVQLQESGSPSLVPSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGCVSSGALTAYN 60
|||||
DB 20 QVQLQESGSPSLVPSQTLSTCTVSGFSLTKYGVSWVRQAPRKALEWVSSIGTSGGLYYN 79
|||||

QY 61 TALQSLSTYTRDTSKQSFSLSSVTTEPTAIYYCAKSVNGDSVPYGLDYWSPGLLTYS 120
|||
DB 80 PALKSRSLSTRDTSKQSVSLSSVTTEPTAIYYCAR-ISSGAPYSIDYWGFLVTVS 138
|||

QY 121 S 121
|
DB 139 S 139

RESULT 15

S54244

Ig mu heavy chain V region precursor - sheep (fragment)

C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)

C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999

C:Accession: S54244

R:Dufour, V.; Nau, F.

submitted to the EMBL Data Library, April 1995

A:Description: Sheep Immunoglobulin mu heavy chain variable region sequence.

A:Reference number: S54225

A:Accession: S54244

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-144 <DUF>

A:Cross-References: EMBL:Z49173; NID:g794129; PIDN:CAA89042.1; PID:g794130

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: Immunoglobulin

F:34-116/Domain: Immunoglobulin homology <IMM>

Query Match

70.4%; Score 432; DB 2; Length 144;

Best Local Similarity 70.6%; Pred. No. 2.2e-30;

Matches 89; Conservative 11; Mismatches 20; Indels 6; Gaps 2;

QY 1 QVQLQESGSPSLVPSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGCVSSGALTAYN 60
|||||
DB 20 QVQLQESGSPSLVPSQTLSTCTVSGFSLTKYGVSWVRQAPRKALEWLSYIYNNCDTDYN 79
|||||

QY 61 TALQSLSTYTRDTSKQSFSLSSVTTEPTAIYYCAKSVNGDSVPY----GLDYWSPGL 115
|||
DB 80 AALKSRSLSTRDTSKQSVSLSSVTTEPTAIYYCTRTDTSARS-GYANGIGGVDFWGRGL 138
|||

QY 116 LTVSS 121
|
DB 139 LTVSS 144

Search completed: August 12, 2002, 09:23:26
Job time: 36 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2002, 09:22:50 ; Search time 15.82 Seconds
(without alignments)
296.148 Million cell updates/sec

Title: US-09-786-015-2
Perfect score: 614
Sequence: 1 QVQLQESGSLVSPQSLTL.....DSVPYGLDYWSPGLLTIVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	59.9	144	1	HY43_MOUSE P01819 mus musculu
2	351	57.2	137	1	HY46_MOUSE P01822 mus musculu
3	338	55.0	116	1	HY45_MOUSE P01821 mus musculu
4	336	54.7	115	1	HY44_MOUSE P01820 mus musculu
5	334.5	54.5	146	1	HY21_HUMAN P06331 homo sapien
6	331.5	54.0	116	1	HY61_MOUSE P18532 mus musculu
7	327	53.3	113	1	HY47_MOUSE P01823 mus musculu
8	320.5	52.2	116	1	HY60_MOUSE P18531 mus musculu
9	318	51.8	117	1	HY26_HUMAN P01825 homo sapien
10	315.5	51.4	135	1	HY02_XENLA P20957 xenopus lae
11	314	51.1	129	1	HY2F_HUMAN P01824 homo sapien
12	311	50.7	117	1	HY62_MOUSE P18533 mus musculu
13	303	49.3	119	1	HY2C_HUMAN P01816 homo sapien
14	294.5	48.0	120	1	HY2B_HUMAN P01815 homo sapien
15	290	47.2	136	1	P20956 xenopus lae
16	289.5	47.1	126	1	HY01_XENLA P01814 homo sapien
17	284	46.3	121	1	HY2J_HUMAN P01771 homo sapien
18	284	46.3	125	1	HY2D_HUMAN P01817 homo sapien
19	282	45.9	121	1	HY01_MOUSE P01745 mus musculu
20	279.5	45.5	122	1	HY03_HUMAN P01762 homo sapien
21	279	45.4	120	1	HY3A_MOUSE P01747 mus musculu
22	278	45.3	115	1	HY3D_HUMAN P01765 homo sapien
23	277.5	45.2	136	1	HY2C_RABIT P01829 oryctolagus
24	275.5	44.9	122	1	HY3H_HUMAN P01769 homo sapien
25	274.5	44.7	116	1	HY3T_HUMAN P01810 homo sapien
26	274.5	44.7	119	1	HY4Q_MOUSE P01810 mus musculu
27	274.5	44.7	136	1	HY16_MOUSE P01783 mus musculu
28	273	44.5	117	1	HY2B_RABIT P01828 oryctolagus
29	272	44.3	121	1	HY2E_HUMAN P01818 homo sapien
30	270.5	44.1	139	1	HY07_MOUSE P01751 mus musculu
31	269	43.8	140	1	HY02_MOUSE P01746 mus musculu
32	269	43.8	142	1	HY01_RAT P01805 rattus norv
33	269	43.8	147	1	HY2H_HUMAN P04438 homo sapien

34	268.5	43.7	119	1	HY37_MOUSE P01807 mus musculu
35	268	43.6	117	1	HY41_MOUSE P01811 mus musculu
36	268	43.6	119	1	HY41_HUMAN P01773 homo sapien
37	267.5	43.6	114	1	HY2A_RABIT P01827 oryctolagus
38	267.5	43.6	118	1	HY3I_MOUSE P06330 mus musculu
39	267.5	43.6	119	1	HY38_MOUSE P01808 mus musculu
40	266.5	43.4	117	1	HY3C_HUMAN P01764 homo sapien
41	266	43.3	117	1	HY42_MOUSE P01812 mus musculu
42	266	43.3	123	1	HY19_MOUSE P01788 mus musculu
43	265	43.2	117	1	HY12_MOUSE P01756 mus musculu
44	265	43.2	118	1	HY39_MOUSE P01809 mus musculu
45	264.5	43.1	120	1	HY50_MOUSE P06329 mus musculu

ALIGNMENTS

```
RESULT 1
ID      HV43_MOUSE      STANDARD;      PRT;      144 AA.
AC      P01819:
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V region MOPC 141 precursor.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=81012133; PubMed=6774258;
RA      Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT      "Two types of somatic recombination are necessary for the generation
RT      of complete immunoglobulin heavy-chain genes.";
RL      Nature 286:676-683(1980).
CC      -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC      DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES ICG2B.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: J00491; AAA8121.1; -.
DR      EMBL: V00768; CAA24149.1; -.
DR      PIR: A02094; G2MS14.
DR      InterPro: IPR003006; IG_MHC.
DR      InterPro: IPR003596; IG_V.
DR      Pfam: PF00047; Ig_1.
DR      SMART: SM00406; IG; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL      1
FT      CHAIN      19
FT      NON_TER      144
SQ      SEQUENCE      144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;
```

Query Match Best Local Similarity 59.9%; Score 368; DB 1; Length 144;
Matches 77; Conservative 16; Mismatches 27; Indels 6; Gaps 3;

```
QY      1 QVQLQESGSLVSPQSLTLCTVSGFSLTKYGVSNVRQAPGKALEMLGCVSGGALTAVN 60
DB      20 QVQLQESGSLVSPQSLTLCTVSGFSLTKYGVSNVRQAPGKALEMLGCVSGGALTAVN 79
QY      61 TALQSRLESTRTSKSQRSLSSVTTEDTATLYYCAKSYN----GDSVY-GLDYWSPGL 115
DB      80 STLKSRLESTRTSKSQRSLSSVTTEDTATLYYCAKSYN----GDSVY-GLDYWSPGL 138
```

OY	116	LITVSS	121
	:		
Dd	139	SVTVSS	144
	RESULT	2	
	HV46_MOUSE		
ID	HVA6_MOUSE	STANDARD:	PRT: 137 AA.
AC	P018622		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	01-AUG-1992 (Rel. 23, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Ig heavy chain V region MOPC 315 precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	NCBI_taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89238351; PubMed=2497341.		
RA	Rifret A., Horne C., Dorrington K.J., Klein M.;		
RT	"Cloning, sequencing and expression of the rearranged MOPC 315 VH		
RL	gene segment.";		
RM	Mol. Immunol. 26:431-434(1989).		
RN	[2]		
RP	SEQUENCE OF 1-31.		
RX	MEDLINE=78094473; PubMed=414225;		
RA	Jilka R.L., Pestka S.;		
RT	"Amino acid sequence of the precursor region of MOPC-315 mouse		
RL	immunoglobulin heavy chain.";		
RM	Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).		
RN	[3]		
RP	SEQUENCE OF 1-21.		
RX	MEDLINE=79148738; PubMed=428562;		
RA	Schechter I., Wolf O., Zemell J., Burstein Y.;		
RT	"Structure and function of immunoglobulin genes and precursors.";		
RL	Fed. Proc. 38:1839-1845(1979).		
RN	[4]		
RP	SEQUENCE OF 19-136.		
RX	MEDLINE=7417073; PubMed=4524622;		
RA	Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;		
RT	"Amino-acid sequence of the variable region of the heavy (alpha)		
RL	chain of a mouse myeloma protein with anti-hapten activity.";		
RM	Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).		
RN	[5]		
RP	REVISION TO 53.		
RX	MEDLINE=77244979; PubMed=268248;		
RA	Hood L., Margolies M.N., Givol D., Zakut R.;		
RT	Unpublished results, cited by:		
RL	Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;		
RM	Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).		
CC	- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA		
CC	PROTEIN THAT HAS ANTI-DINTROPHENYL ACTIVITY.		
CC	-----		
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CC	or send an email to license@isb-slb.ch).		
CC	-----		
DR	EMBL; M27638; AAA61337.1; .		
DR	EMBL; X07880; CAA30727.1; .		
DR	PIR; PLO102; AVMS35.		
DR	InterPro; IPRO03006; IG_MHC.		
DR	InterPro; IPRO03596; IG_V.		
DR	Pfam; PF00047; Ig_1.		
DR	SMART; SM00406; IGV_1.		
KW	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	
FT	CHAIN	19	137
FT	DOMAIN	19	48
			IG HEAVY CHAIN V REGION MOPC 315.
			FRAMEWORK-1.

FT	DOMAIN	49	54		COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	55	68		FRAMEWORK-2.
FT	DOMAIN	69	84		COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	85	116		FRAMEWORK-3.
FT	DOMAIN	117	126		COMPLEMENTARITY-DETERMINING-3.
FT	DISULFID	127	137		FRAMEWORK-4.
FT	CONFLICT	40	114		BY SIMILARITY
FT	CONFLICT	15	15		G -> GG (IN REF. 1; CAA30727).
FT	CONFLICT	15	15		G -> H (IN REF. 2).
FT	CONFLICT	77	78		GY -> YG (IN REF. 4).
FT	CONFLICT	102	102		N -> D (IN REF. 4).
FT	CONFLICT	123	123		MISSING (IN REF. 4).
FT	NON_TER	137	137		
SQ	SEQUENCE	137 AA;	15399 MW;		FBI3828304CB8LDC CRC64;
<hr/>					
Query Match					
Best Local Similarity					
Matches 72; Conservative 17; Mismatches 27; Indels 6; Gaps 3;					
<hr/>					
OY	2 VOLDSEGSVLKPPSQTLSICTVSGFSLT-K-YGVSWRQAQPKALEWLGVSAGALTRAYN 60				
Dd	20 VOLQSGEGVLKPSQSLSITCSVTGXSTISGFWMNMIRPGPNKLKLEMGFKIKYDSDNGYN 79				
OY	61 TALQRSLVTDTSKSQSSLSISTTTTDTTAIYYAKAVNSDSVP-YGLDWSPBLLTLTY 119				
Dd	80 PSLKNRVSIPTDRSENOPFLKLNSTVEDTATYYCA---GDNDHLYYEDYGQGCTTLTV 135				
OY	120 SS 121				
Dd	136 SS 137				
<hr/>					
RESULT	3				
HV45_MOUSE	STANDARD:	PRT,	116 AA.		
ID AC	P01821;				
Dt	21-JUL-1986 (Rel. 01, Created)				
Dt	21-JUL-1986 (Rel. 01, Last sequence update)				
Dt	15-JUN-1999 (Rel. 38, Last annotation update)				
De	Ig heavy chain v region MC101 precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=82075900; PubMed=6273429;				
RA	Katataka T., Nikaido T., Miyata T., Moriaki K., Honjo T.,				
RT	"The nucleotide sequences of rearranged and germ-line immunoglobulin				
RL	VH genes of a mouse myeloma MC101 and evolution of VH genes in				
J. Biol. Chem.	257:277-285(1982)."				
<hr/>					
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DR	EMBL; J00502; AAA38515.1; .				
DR	PIR; A02096; GIMS10.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; Igv; 1.				
KV	Immunoglobulin V region; Signal.				
FT	SIGNAL	1	19		
FT	CHAIN	20	116		IG HEAVY CHAIN V REGION MC101.
FT	NON_TER	116	116		
SQ	SEQUENCE	116 AA;	12593 MW;		8079A6EE7C552B3E CRC64;

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Query Match          55.0%; Score 338; DB 1; Length 116;
Best Local Similarity 64.9%; Pred. No. 3.1e-27;
Matches 63; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

OY 1 QVQLQESGPELVPSQTLSTCTVSGFSLTKRYGVSWVROAPGKALEWLGVSAGLTAYN 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 QVQLKSGPELVPSQSLSTCTVSGFSLTKRYGVSWVROAPGKALEWLGVSAGLTAYN 79

OY 61 TALQSRISVTRDTSKQSFSLSSVTEDTAIYYCA 97
    ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 AAFISRLISKDNKSKQVFPKMNLSQNDTAIYYCA 116

RESULT 4
HV44_MOUSE STANDARD; PRT; 115 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V region PJ14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Makl R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes."
RL Nature 285:676-683(1980).
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CC -----
DR EMBL: V00767; CAA24148.1; -
DR PIR: A02095; HYMS14.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT NON_TER 115
FT SEQUENCE 115 AA; 12447 MW; 7569DDA4843D500 CRC64;

Query Match          54.7%; Score 336; DB 1; Length 115;
Best Local Similarity 66.7%; Pred. No. 4.9e-27;
Matches 64; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

OY 1 QVQLQESGPELVPSQTLSTCTVSGFSLTKRYGVSWVROAPGKALEWLGVSAGLTAYN 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 20 QVQLKSGPELVPSQSLSTCTVSGFSLTKRYGVSWVROAPGKALEWLGVSAGLTAYN 79

OY 61 TALQSRISVTRDTSKQSFSLSSVTEDTAIYYCA 96
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 80 SALKSRISISKDNKSKQVFLKMNLSQTDTAIYYCA 115

RESULT 5
HV21_HUMAN STANDARD; PRT; 146 AA.
AC F06331;

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DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region."
RL Gene 33:181-189(1985).
DR PIR: A02101; G1H0R2.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT DOMAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146
FT SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match          54.5%; Score 334.5; DB 1; Length 146;
Best Local Similarity 52.4%; Pred. No. 9.2e-27;
Matches 66; Conservative 20; Mismatches 35; Indels 5; Gaps 1;

OY 1 QVQLQESGPELVPSQTLSTCTVSGFSLTKRYGVSWVROAPGKALEWLGVSAGLTAYN 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 21 QVQLQAGAGLVKPSRSLSTCAVFGSFGSYKSWTRQPRGRLEWLGELNHSGRINRK 80

OY 61 TALQSRISVTRDTSKQSFSLSSVTEDTAIYYCAKSV-----NGDSVPYGLDYNSPGL 115
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 81 TSLKSRVITSLDPSKSNFSLKSSVTADTAIYYCARGLLRGGNVDVYYGMDPMVQGT 140

OY 116 LITVSS 121
    :|||||
DB 141 TVTVSS 146

RESULT 6
HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR PIR: J0508; HVMS1B.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.

```

0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
0C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP
RN
SEQUENCE.
QX MEDLINE=77242302; PubMed=407927;

RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
 RT "Amino acid sequence of the VH region of a human myeloma
 RL Immunoglobulin (IgG New).";
 RN Biochemistry 16:3412-3420(1977).
 RP [2]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE-78066916; PubMed-618887;
 RA Saul F.A., Amzel L.M., Poljak R.J.;
 RT "Preliminary refinement and structural analysis of the Fab fragment
 from human immunoglobulin new at 2.0-A resolution.";
 RL J. Biol. Chem. 253:385-397(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR PIR: A02100; GIHUNM.
 DR PDB: 7FAB; 31-JAN-94.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT STRAND 3 7
 FT TURN 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT TURN 57 59
 FT STRAND 61 63
 FT TURN 64 66
 FT STRAND 67 72
 FT TURN 73 76
 FT STRAND 77 82
 FT TURN 87 89
 FT STRAND 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12790 MM; 2DN47B509562D237 CRC64;

Query Match 51.8%; Score 318; DB 1; Length 117;
 Best Local Similarity 53.7%; Pred. No. 3.2e-25;
 Matches 65; Conservative 21; Mismatches 31; Indels 4; Gaps 1;

OY 1 OVQLQSGPSLVKPSQTLSTCTVSGFSLTKYGVSWVROAPGKALEMLGVSSESGALTAYN 60
 DB 1 OVQLQSGPSLVKPSQTLSTCTVSGFSLTKYGVSWVROAPGKALEMLGVSSESGALTAYN 60
 OY 61 TALQSLVTRDTSKSQFSLSSVTEEDTAIYYCAKSVNGDSVPYGLDWSGILLTVSS 120
 DB 61 TPLKSHVTLVDTSKNQFSLRLSVTAADTAIVYVCARNL-----IACIDVWGSGSLTVTS 116
 OY 121 S 121
 DB 117 S 117

RESULT 10
 HVO2_XENLA STANDARD; PRT; 135 AA.
 AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region XIG14 precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88176921; PubMed-2451244;
 RA Schwager J., Mikoryak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
 from cDNA sequence: implications for evolution of immunoglobulin
 RT domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
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 CC -----
 DR EMBL: J03632; AAA49791.1; -.
 DR PIR: B31933; B31933.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL 1 18
 FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
 FT NON_TER 135 135
 SQ SEQUENCE 135 AA; 15080 MM; EBC467105C00732E CRC64;

Query Match 51.4%; Score 315.5; DB 1; Length 135;
 Best Local Similarity 47.5%; Pred. No. 6.7e-25;
 Matches 56; Conservative 26; Mismatches 33; Indels 3; Gaps 1;

OY 4 LOESGPSLVKPSQTLSTCTVSGFSLTKYGVSWVROAPGKALEMLGVSSESGALTAYN 63
 DB 21 LOESGPGTVKPSSESLRTECTVSGFELSSYMHMIRQPPGKLEWIVYATGSLTALD 80
 OY 64 QSRSLVTRDTSKSQFSLSSVTEEDTAIYYCAKSVNGDSVPYGLDWSGILLTVSS 121
 DB 81 KNRVITTKDNGKKQVYLVQNGMEVKDPTAMYYCAREY---ASGYNFDYWGSGTVTVTS 135

RESULT 11
 HVE2_HUMAN STANDARD; PRT; 129 AA.
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region WAH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-8222235; PubMed-6806818;
 RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 RT immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 CC PROTEIN.
 DR PIR: A02099; D2HUMA.
 DR HSSP: P01825; 7FAB.
 DR GlycoSuiteDB: P01824; -.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00406; IgV; 1.

KM Immunoglobulin V region.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 51.1%; Score 314; DB 1; Length 129;
 Best Local Similarity 49.2%; Pred. No. 9e-25;
 Matches 65; Conservative 22; Mismatches 31; Indels 14; Gaps 3;

OY 1 QVOLOESGSLVKSQTLSTCTVSGFSL--TRYGSVWRQAPGKALEMLGVSAGALTA 58
 DB 1 RLOQESGGLVKSQTLSTCTVSGFPIRRCYIGWMIROPKGLKLEMLGVSAGALTA 60
 OY 59 YNTALOSRLSVTRDTSKQSFSLSSVTTEEDTAIYYCAKSVNGDSVPY-----GLD 109
 DB 61 YNLSLGRVYISVDTSRNOFSLNLRMSAADTFAMYCAR---GNPPPYDIGTSDGDID 117
 OY 110 YMSPGLLTVSS 121
 DB 118 VWGQGTTHVSS 129

RESULT 12
 HV62_MOUSE STANDARD; PRT; 117 AA.
 AC P18533;

DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 733 precursor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malpietro U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RT J. Exp. Med. 169:2007-2019(1989).
 RL PIR: J0510; HVMS73.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1 18
 FT SIGNAL 19 117 IG HEAVY CHAIN V REGION 733.
 FT DISULFID 40 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 50.7%; Score 311; DB 1; Length 117;
 Best Local Similarity 59.2%; Pred. No. 1.6e-24;
 Matches 58; Conservative 19; Mismatches 19; Indels 2; Gaps 1;

OY 2 VOLOESGSLVKSQTLSTCTVSGFSLT--KYGSVWRQAPGKALEMLGVSAGALTA 59
 DB 20 VLOQESGGLVKSQTLSTCTVSGFISITIGNRMWMIQFPKNKLEMLGVSAGALTA 79
 OY 60 NTALOSRLSVTRDTSKQSFSLSSVTTEEDTAIYYCAK 97
 DB 80 NPSPKSRITTRDTSKNOFLEKNSLTADDTATYYCAR 117

RESULT 13
 HV2C_HUMAN STANDARD; PRT; 119 AA.
 AC P01816;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region DAW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 heavy chains."
 RT Biochem. J. 117:641-660(1970).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM THE
 SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
 DR PIR: A02091; GIHDM.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT NON_TER 119 119 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 49.3%; Score 303; DB 1; Length 119;
 Best Local Similarity 51.2%; Pred. No. 1e-23;
 Matches 63; Conservative 22; Mismatches 32; Indels 6; Gaps 2;

OY 1 QVOLOESGSLVKSQTLSTCTVSGFSLT--KYGSVWRQAPGKALEMLGVSAGALTA 58
 DB 1 QVTLRESGALVAPROTLLTCTFSGFSLSGETWCVAMIRPQKGLKLEMLDNDKY 60
 OY 59 YNTALOSRLSVTRDTSKQSFSLSSVTTEEDTAIYYCAKSVNGDSVPYGLDTPSGLLT 118
 DB 61 YGASLETRLAVSKDTSKNOVLSMNTVGPDTATYYCARSCSQY---FDYWGQGLT 116
 OY 119 VSS 121
 DB 117 VSS 119

RESULT 14
 HV2B_HUMAN STANDARD; PRT; 120 AA.
 ID HV2B_HUMAN
 AC P01815;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region COR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 heavy chains."
 RT Biochem. J. 117:641-660(1970).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ICG1 MYELOMA
 PROTEIN.
 DR PIR: A02089; GIHUCO.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT MOD_RES 1 1
 FT DISULFID 22 94 PYRROLIDONE CARBOXYLIC ACID.

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099NG4
ID 099NG4 PRELIMINARY: PRT: 121 AA.
AC 099NG4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE SINGLE CHAIN FV (FRAGMENT).
OS Mus musculus (Mouse).
OC Plasmid pHEM1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
RA Bausch W., Kola A., Klos A., Koehl J.;
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL: AJ222590; CNA10890.1; -.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00409; Ig_1.
DR SMART: SM00406; IgV_1.
DR SMART: SM00410; Ig_Like; 1.
KW Plasmid.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13255 MW; D293E4EB8C959D5B CRC64;

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Query Match          59.7%; Score 366.5; DB 11; Length 121;
Best Local Similarity 60.0%; Pred. No. 2.7e-30;
Matches 75; Conservative 14; Mismatches 27; Indels 9; Gaps 2;

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QY 1 QVQLQESGSPSLVPSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEMLGCVSSGALTAYN 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 QVQLKESGPGVLVAPSGSLSTCTVSGFPLTSHGVSWVRQPGKALEMLGIVIMDGMTKYH 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TALQSLRYTRPTSKQSFSLSSVTEPTAIYYCA----KSYNGDSVPRGLDYSPGLL 116
   :||| ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 SALISRLISIKDNSKQVFLKNSLQTEDTATYTCARHYKYKAN-----YAMDYWGQGT 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 117 LTVSS 121
   :||| |||||
DB 116 LTVSS 120

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RESULT 3
Q96EYO PRELIMINARY: PRT: 613 AA.
AC 096EYO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:20337).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILLS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011857; AAH11857.1; -.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

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Query Match          58.9%; Score 361.5; DB 4; Length 613;
Best Local Similarity 58.7%; Pred. No. 6.9e-29;
Matches 74; Conservative 17; Mismatches 24; Indels 11; Gaps 2;

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QY 1 QVQLQESGSPSLVPSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEMLGCVSSGALTAYN 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 QVQLQESGPGVLVAPSGSLSTCTVSGSISYWSVRQPGKALEMLGIVIMDGMTKYH 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TALQSLRYTRPTSKQSFSLSSVTEPTAIYYCAKSYNGDSVPRGLDYSPGLL 115
   :||| ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 PSLKSRVTMSVDTSKNQFSLKLSVTAAADTAYYYCA-----SQPHELPTVGLFTWGQGT 133
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 116 LTVSS 121
   :||| |||||
DB 134 LTVSS 139

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RESULT 4
Q9UL73 PRELIMINARY: PRT: 119 AA.
AC 09UL73;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
   (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035041; AAD56277.1; -.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;

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Query Match          58.3%; Score 358; DB 4; Length 119;
Best Local Similarity 57.9%; Pred. No. 2e-29;
Matches 70; Conservative 18; Mismatches 31; Indels 2; Gaps 1;

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QY 1 QVQLQESGSPSLVPSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEMLGCVSSGALTAYN 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 QVQLQESGPGVLVAPSGSLSTCTVSGSISYWSVRQPGKALEMLGIVIMDGMTKYH 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TALQSLRYTRPTSKQSFSLSSVTEPTAIYYCAKSYNGDSVPRGLDYSPGLLTVS 120
   :||| ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 PSLKSRVTISVDRSKNQFSLKLSVTAAADTAYYYCAKLSNMG--PYFPDYWGQGTLYVS 118
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 S 121
   :||| |||||
DB 119 S 119

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```

RESULT 5
Q95973 PRELIMINARY: PRT: 150 AA.
AC 095973;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)

```

Query Match	54.5%	Score 334.5	DB 4	Length 150
Best Local Similarity	54.5%	Pred. No. 7e-27		
Matches 67; Conservative	20;	Mismatches 29;	Indels 7;	Gaps 2

RESULT 6
Q9BQ8
ID Q9BQ8
PRELIMINARY;
PRT: 597 AA.

AC Q9BOB8:01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=RHABDOMYOSARCOMA;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPHOMA;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AAH06180.1; -
 DR EMBL; BC001872; AAH01872.1; -
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR003597; Iq.
 DR InterPro; IPR003597; Iq-cl.
 DR InterPro; IPR003600; Iq-like.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003596; Iq_v.

Query Match	54.28;	Score 333;	DB 4;	Length 597;
Best Local Similarity	52.08;	Pred. No. 5.8e-26;		
Matches 65; Conservative	20;	Mismatches 36;	Indels 4;	Gaps 1;

RESULT 7
Q99M22 PRELIMINARY;
ID Q99M22 PRT; 479 AA.

RC	TISSUE-MAMMARY TUMOR.	WAP-TGF ALPHA MODEL.	7 MONTHS OLD,	GROSS
RC	TISSUE-?			
RC	TISSUE-?			
RA	Strausberg R.?			

Query Match	53.7%	Score 330;	DB 11;	Length 479;
Best Local Similarity	54.0%	Pred. No. 9e-26;		
Matches 67; Conservative	20;	Mismatches 25;	Indels 12;	Gaps 3;

[illegible]

QY 118 TVSS 121
DB 132 TVSA 135

RESULT 8

Q9UL96 PRELIMINARY; PRT; 121 AA.

AC Q9UL96; PRELIMINARY; PRT; 121 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
RU Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035018; AAD56254.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 53.6%; Score 329; DB 4; Length 121;
Best Local Similarity 54.5%; Pred. No. 2e-26;
Matches 67; Conservative 20; Mismatches 32; Indels 4; Gaps 2;

QY 1 OVOLOESGSLVPSQTLSTCTVSGFSLTKYGVSWRQAPGKALEWLGVSAGALTA 58
DB 1 QITLKESGSLVPSQTLSTCTVSGFSLTKYGVSWRQAPGKALEWLGVSAGALTA 60
QY 59 YNTALQSLVTRDTSKQPSLSVTTEDTAIYCAKSVNGDSVPYGLDWSFGLLT 118
DB 61 YSPLSKSRITITKDTSKNQVDLTMTPMDPTATFYCAHRSKSGDG--YTFDYGQGTLT 118
QY 119 VSS 121
DB 119 VSS 121

RESULT 9

Q9BU10 PRELIMINARY; PRT; 597 AA.

AC Q9BU10; PRELIMINARY; PRT; 597 AA.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 65.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, LYMPHOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01825; 7FAB.

QY 1 OVOLOESGSLVPSQTLSTCTVSGFSLTKYGVSWRQAPGKALEWLGVSAGALTA 60
DB 20 QVOLOQWAGALIKPSELTSLTCGYGSGFYGSWSWIRPPGKLEWIGETINHSSTYN 79
QY 61 TALQSLVTRDTSKQPSLSVTTEDTAIYCAKSVN---GDSVPYGLDWSFGLL 116
DB 80 PSLKSRITISVDTSKQPSLSVTTEDTAIYCAKSVN---GDSVPYGLDWSFGLL 139
QY 117 TVSS 121
DB 140 TVSS 144

DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR00047; Ig; 5.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAPAF8FB7E055851 CRC64;

Query Match 53.6%; Score 329; DB 4; Length 597;
Best Local Similarity 52.0%; Pred. No. 1.5e-25;
Matches 65; Conservative 19; Mismatches 37; Indels 4; Gaps 1;

QY 1 OVOLOESGSLVPSQTLSTCTVSGFSLTKYGVSWRQAPGKALEWLGVSAGALTA 60
DB 20 QVOLOQWAGALIKPSELTSLTCGYGSGFYGSWSWIRPPGKLEWIGETINHSSTYN 79
QY 61 TALQSLVTRDTSKQPSLSVTTEDTAIYCAKSVN---GDSVPYGLDWSFGLL 116
DB 80 PSLKSRITISVDTSKQPSLSVTTEDTAIYCAKSVN---GDSVPYGLDWSFGLL 139
QY 117 TVSS 121
DB 140 TVSS 144

RESULT 10

Q96AA6 PRELIMINARY; PRT; 618 AA.

AC Q96AA6; PRELIMINARY; PRT; 618 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 67.8 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, AND LYMPHOMA;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.1; -.
KW Hypothetical protein.
SQ SEQUENCE 618 AA; 67758 MW; 96BBD4C7C696E0A6 CRC64;

Query Match 53.6%; Score 329; DB 4; Length 618;
Best Local Similarity 52.0%; Pred. No. 1.6e-25;
Matches 65; Conservative 19; Mismatches 37; Indels 4; Gaps 1;

QY 1 OVOLOESGSLVPSQTLSTCTVSGFSLTKYGVSWRQAPGKALEWLGVSAGALTA 60
DB 20 QVOLOQWAGALIKPSELTSLTCGYGSGFYGSWSWIRPPGKLEWIGETINHSSTYN 79
QY 61 TALQSLVTRDTSKQPSLSVTTEDTAIYCAKSVN---GDSVPYGLDWSFGLL 116
DB 80 PSLKSRITISVDTSKQPSLSVTTEDTAIYCAKSVN---GDSVPYGLDWSFGLL 139
QY 117 TVSS 121
DB 140 TVSS 144

RESULT 11

Q96KX8

ID Q96KX8 PRELIMINARY: PRT: 496 AA.
AC Q96KX8:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 53.4 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
KW Hypothetical protein.
SQ SEQUENCE 496 AA: 53391 MW: D346929849040D69 CRC64;

Query Match 52.7%; Score 323.5; DB 4; Length 496;
Best Local Similarity 53.2%; Pred. No. 4.4e-25;
Matches 66; Conservative 20; Mismatches 35; Indels 3; Gaps 2;

QY 1 QVQLQESGPSTLVKPSQTLSTCTVSGFSL--TKYGVSWYRQAPGKALEWLGVSAGALTA 58
DB 20 QVQLQESGPGLVKSEETISLTCTVSGGSISSSYWGMRQPGKLEMIATFYSGITY 79
QY 59 YNTALQSLRSLVTRDTSKQSFSLSSVTTEDTAIYCAKSVNGDSVPYG-LDYSPGLLL 117
DB 80 YNPISKRSVTVISVDTSKNQLSLKVRSAADPAVYCAHGRSGRGTAIDYWGCGTLY 139
QY 118 TVSS 121
DB 140 TVSS 143

RESULT 12
ID Q9UL75 PRELIMINARY: PRT: 122 AA.
AC Q9UL75:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; Pubmed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035039; AAD56275.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA: 13719 MW: 56CDB0612586A6529 CRC64;

Query Match 51.7%; Score 317.5; DB 4; Length 122;
Best Local Similarity 52.0%; Pred. No. 3.1e-25;
Matches 66; Conservative 20; Mismatches 30; Indels 11; Gaps 4;

QY 1 QVQLQESGPSTLVKPSQTLSTCTVSGFSLTKYGV---SWYRQAPGKALEWLGVS--SSGAL 56
DB 1 QVQLQESGPGLVKPSQTLSTCTVCAISGDSVSNNAAMNWRQSPRLKEMIGRIYYSKRY 60
QY 57 YNTALQSLRSLVTRDTSKQSFSLSSVTTEDTAIYCAKSVN--GDSVPYGLDYWSPG 114
DB 61 NDYRVSKRSRITINPDTSKNOFSLQLNSVTPEDTAVYCAKDLELLGQ-----FDWCGG 115
QY 115 LTVSS 121
DB 116 LTVSS 122

RESULT 13
ID Q9Y509 PRELIMINARY: PRT: 147 AA.
AC Q9Y509:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; Pubmed-7475288;
RA Cao J., Vesic R.A., Rettig M.B.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14359.1; -.
DR HSSP; P01772; 2E84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
SQ SEQUENCE 147 AA: 15768 MW: 8489FCMAA7BC925C CRC64;

Query Match 49.8%; Score 305.5; DB 4; Length 147;
Best Local Similarity 48.4%; Pred. No. 6.7e-24;
Matches 61; Conservative 25; Mismatches 35; Indels 5; Gaps 3;

QY 1 QVQLQESGPSTLVKPSQTLSTCTVSGFSLTKYGVSWYRQAPGKALEWLGVS--SGALTA 59
DB 1 QVHLVSGGGVYQPGKSLRLSCASGFTSTYGMWYRQAPGKGLDVALISDVGSTGY 60
QY 60 NVALQSLRSLVTRDTSKQSFSLSSVTTEDTAIYCAKSVN-GDSVPY---GLDYSPGL 115
DB 61 AGSVKGRFTISRDNSKNTLYQMTSLRVEDTAIVYCAKNGYDSVGYVYAGIDYWGQGT 120
QY 116 LTVSS 121
DB 121 LTVSS 126

RESULT 14
ID Q96BB9 PRELIMINARY: PRT: 597 AA.
AC Q96BB9:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

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Tue Aug 13 08:57:25 2002

OM of: US-09-786-015-4 to: GenEmbl:* out_format : pfs

Date: Aug 12, 2002 10:39 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-O=MODEL-frame+_p2n.model -DEV=xlp  
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-DB=genembl -QEMT=fastlap -SUFFIX=p2n.rge -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blsnum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09786015 @CGN1_1.7012 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query: US-09-786-015-4  
Query length: 111  
Database: GenEmbl:*  
Database sequences: 1797656  
Search length: 1873333701  
Search time (sec): 1937.690000
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score_list:

Sequence	Strd Orig	EScore	Len	Documentation
gb.com:BTU32261	+	455.00	818.22	393
gb.com:AF172696	+	451.50	813.46	330
gb.com:AF172691	+	447.00	805.26	333
gb.com:AF172689	+	446.00	803.46	333
gb.com:AF172688	+	445.00	801.66	333
gb.com:AF015795	+	444.50	800.75	333
gb.com:AF015792	+	443.50	798.94	333
gb.com:AF172684	+	442.00	796.42	333
gb.com:AF172686	+	441.50	795.42	330
gb.com:AF172687	+	441.50	795.42	330
gb.com:AF015798	+	440.50	793.53	333
gb.com:AF015799	+	440.50	793.53	333
gb.com:AF015801	+	440.50	793.53	333
gb.com:AF172688	+	439.50	791.64	336
gb.com:AF172693	+	439.00	790.82	333
gb.com:BTU32250	+	439.00	789.21	399
gb.com:AF172700	+	438.50	790.12	324
gb.com:AF015797	+	435.00	783.69	330
gb.com:AF172697	+	433.00	779.99	333
gb.com:AF109697	+	430.00	774.66	330
gb.com:BTU31106	+	430.00	773.10	393
gb.com:BTU32255	+	429.50	773.68	333
gb.com:AF015791	+	429.50	773.68	333
gb.com:AF015793	+	429.50	773.68	333
gb.com:AF172698	+	429.50	773.68	336
gb.com:AF023841	+	429.00	772.70	336
gb.com:BTU32254	+	429.00	771.39	393
gb.com:AF172699	+	428.50	771.79	336
gb.com:AF015796	+	428.00	771.05	330
gb.com:AF023843	+	427.00	769.25	330
gb.com:BTU32249	+	425.00	764.08	393
gb.com:AF172695	+	424.00	763.75	333
gb.com:AF172692	+	422.50	761.13	330
gb.com:BTU32250	+	422.50	760.97	336
gb.com:AF015800	+	421.50	759.24	333
gb.com:AF172685	+	420.00	756.37	339
gb.com:AF040919	+	418.00	748.64	538
gb.com:AF172682	+	417.00	751.12	333
gb.com:AF015809	+	416.00	749.40	330
gb.com:AF172701	+	416.00	749.40	333

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gb.com:BTU012803 + 415.50 748.33 2.5e-33 336 | AU012803 Bos taurus mRNA for  
gb.com:BTU11633 + 414.00 744.72 4.0e-33 332 | U11633 Bos taurus B11 cell-1-1  
gb.com:AF172694 + 413.00 743.73 4.5e-33 339 | AF172694 Ovis aries clone 47  
gb.com:BTU012804 + 412.50 742.76 5.1e-33 342 | AU012804 Bos taurus mRNA for  
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seq_documentation_block:

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LOCUS BTU32261 393 bp mRNA linear MAM 25-APR-1996  
DEFINITION Bos taurus clone 16 Immunoglobulin lambda light chain variable  
region (Vlambda) mRNA, partial cds.  
ACCESSION U32261  
VERSION U32261.1 GI:1276622  
KEYWORDS
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SOURCE

ORGANISM

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cow.  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
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REFERENCE

```
1 (bases 1 to 393)  
Ivanov,V.N., Karginov,V.A., Morozov,I.V. and Gorodetsky,S.I.  
Molecular cloning of a bovine immunoglobulin lambda chain cDNA  
Gene 67 (1), 41-48 (1988)  
88329743
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REFERENCE

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2 (bases 1 to 393)  
Jackson,T., Morris,B.A. and Sanders,P.G.  
Nucleotide sequences and expression of cDNAs for a bovine  
anti-testosterone monoclonal IgG1 antibody  
Mol. Immunol. 29 (5), 667-676 (1992)  
92261635
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AUTHORS

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3 (bases 1 to 393)  
Sincclair,M.C., Glitchist,J. and Aitken,R.  
Molecular characterization of bovine V lambda regions  
J. Immunol. 155 (6), 3068-3078 (1995)  
95403981
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REFERENCE

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4 (bases 1 to 393)  
Aitken,R.  
Direct Submission  
Submitted (25-JUL-1995) Robert Aitken, Microbiology, Institute of  
Biomedical and Life Sciences, University of Glasgow, Joseph Black  
Building, Glasgow G12 80Q, UK  
Location/Qualifiers  
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sig_peptide

CDS

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mat_peptide  
misc_feature
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misc_feature 241..336
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    Percent Similarity: 93.578      Percent Identity: 81.651

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US-09-786-015-4 x BTU32261 ..

Align seg 1/1 to: BTU32261 from: 1 to: 393

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67 CAGGCTGTGCTGACTCAGCCGCTCCTCGTGGGCTCCGAGGCGCAGAG 116
17 gvalSerllethrcysSerGlySerSerSeraSnlleGlyGlySanaIat 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
117 GGTCTCCATCCTGCTGCTGGAAGCAGCAGCAAGCTGTGCACTGGCAATT 166
34 yfValGlyTrpTyrGlnGlnValProGlySeraIaProArgLeuLeuile 50
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167 ATGTAGCTGTGCTCCACAGATCCAGATGCGCCGCCAGAACCTCTATC 216
217 TATGTGTGGACAGTCAGAGCTCGGGGGTCCCGACGATCTCCGGCTC 266
51 SerIaIaThrAspArgAlaSerGlylleProAspArgPheSerGlyse 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
217 TATGTGTGGACAGTCAGAGCTCGGGGGTCCCGACGATCTCCGGCTC 266
67 fArgSerGlySnaThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
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267 CAGGCTGTGGAACACAGCAGCCCTGACCATCAGCTCGCTCAGGCTGAG 316
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
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317 ACGAGGCGGATATTTCGTGCATCTTATCAGAGTAGTAACACAGCTGTG 366
101 PheGlySerGlyThrArgLeuThrVal 109
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367 TTCGGCAGCGGACACACACTGACCGCTC 393

seq_name: gb_com:AF172696

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LOCUS      AF172696                330 bp      mRNA      linear      MAM 29-AUG-1999
DEFINITION Ovis aries clone 53 immunoglobulin light chain variable region
            (IGLV) mRNA, partial cds.
ACCESSION  AF172696
VERSION    AF172696.1      GI:5802439
KEYWORDS
SOURCE     sheep.
ORGANISM   Ovis aries
            Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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REFERENCE
AUTHORS    1 (bases 1 to 330)
            White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE       A single-chain variable region immunoglobulin library from the
            abomasal lymph node of sheep infected with the gastrointestinal
            nematode parasite Haemonchus contortus
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 330)
AUTHORS    White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE       Direct Submission
JOURNAL     Submitted (26-JUL-1999) School of Veterinary Science, The Centre
            for Animal Biotechnology, The University of Melbourne, Parkville,
            Melbourne, Victoria 3052, Australia
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ORIGIN

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    Percent Similarity: 91.892      Percent Identity: 82.883

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US-09-786-015-4 x AF172696 ..

Align seg 1/1 to: AF172696 from: 1 to: 330

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1 CAGGCTGTGCTGACTCAGCCGCTCCTCGAGTCCGAGTCCCTCGGCGCAGAG 50
17 gvalSerllethrcysSerGlySerSerSeraSnlleGlyGlySanaIat 34
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51 GGTCTCCATCCTGCTGCTGGAAGCAGCAGCAACATC...GGGCTGTGTT 97
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98 ATGTAGCTGTGCTCCACAGATCCAGATGCGCCGCCAGAACCTCTCTATC 147
148 TATATTGCAACCATTCGAGCCTCGGGGGTCCCGACGATCTCCGGCTC 197
51 SerIaIaThrAspArgAlaSerGlylleProAspArgPheSerGlyse 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
148 TATATTGCAACCATTCGAGCCTCGGGGGTCCCGACGATCTCCGGCTC 197
67 fArgSerGlySnaThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
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84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
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248 ACGAGGCGGATATTTCGTGCATCTTATCAGAGTAGTAACAGTATGATATT 297
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seq_name: gb_com:AF172691
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DEFINITION Ovis aries clone 81 immunoglobulin light chain variable region
            (IGLV) mRNA, partial cds.
ACCESSION  AF172691
VERSION    AF172691.1  GI:5802429
KEYWORDS
SOURCE     sheep.
ORGANISM   Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Caprinae; Ovis.
REFERENCE  1 (bases 1 to 333)
AUTHORS   White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE     A single-chain variable region immunoglobulin library from the
            abomasal lymph node of sheep infected with the gastrointestinal
            nematode parasite Haemonchus contortus
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 333)
AUTHORS   White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE     Direct Submission
            Submitted (26-JUL-1999) School of Veterinary Science, The Centre
            for Animal Biotechnology, The University of Melbourne, Parkville,
            Melbourne, Victoria 3052, Australia
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BASE COUNT      63 a      102 c      90 g      78 t

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Quality:      447.00      Length:      111
Ratio:        4.382      Gaps:        0
Percent Similarity:  91.892      Percent Identity:  79.279

alignment_block:
US-09-786-015-4 x AF172691 ..

Align seg 1/1 to: AF172691 from: 1 to: 333

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251 ACGAGGCCGATTATTAATGTCATCTATGACACACAGTAGCATGTGT 300
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101 PheGlySerGlyThrArgLeuThrValLeuGly 111
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301 TTCGGCAGCGGAGCCAGCGTACGCTCGGT 333

seq_name: gb_om:AF172690

seq_documentation_block:
LOCUS      AF172690                333 bp    mRNA    linear    MAM 29-AUG-1999
DEFINITION Ovis aries clone 100 immunoglobulin light chain variable region
            (IGLV) mRNA, partial cds.
ACCESSION  AF172690
VERSION    AF172690.1  GI:5802427
KEYWORDS
SOURCE     sheep.
ORGANISM   Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Caprinae; Ovis.
REFERENCE  1 (bases 1 to 333)
AUTHORS   White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE     A single-chain variable region immunoglobulin library from the
            abomasal lymph node of sheep infected with the gastrointestinal
            nematode parasite Haemonchus contortus
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 333)
AUTHORS   White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE     Direct Submission
            Submitted (26-JUL-1999) School of Veterinary Science, The Centre
            for Animal Biotechnology, The University of Melbourne, Parkville,
            Melbourne, Victoria 3052, Australia
FEATURES
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            /db_xref="GI:5802428"
            /translation="QAVLTQPPSSVSKSLGQSVITSCGSSSNVGYGNVGMFOPLIGS
            APRVLIVGAASRASGVPPDRFGSSRSNTATLTITSLQADEADYICASYDSSSGAFG
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BASE COUNT      63 a      100 c      94 g      76 t

ORIGIN
alignment_scores:
Quality:      446.00      Length:      111
Ratio:        4.330      Gaps:        0
Percent Similarity:  92.793      Percent Identity:  79.279

alignment_block:
US-09-786-015-4 x AF172690 ..

Align seg 1/1 to: AF172690 from: 1 to: 333

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1  GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
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1  CAGCGTGTGCTGACTCAGCCGCTCCGTCGTCAGATCCCGGCCAGAG 50
17  GValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaT 34
51  TGCTCCATCACTGCTGCTGGAACAGCAGCAGCAGCTTGGAATGCTAAT 100
34  yrValGlyTyrGlnGlnValProGlySerAlaProArgLeuLeuLe 50
101 ATGTGGGCTGCTCCACACAGCTCCCTGATCAGCCCCCAACTCCTCAT 150
51  SerAlaThrThrAspArgAlaSerGlyTyrLeuProAspArgPheSerGly 67
151 TATGTGTACACCAATCGAGCTCGGGGCTCCCGACGATTCCTCGGCTC 200
67  rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
17  GValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaT 34

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51 TGTCTCCATCACTGCTCTGGAGCAGTAGCAGCTGTGATATGTAATT 100
34 YVVALGTYPTPLTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
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101 ATGTAGTGTGTTCACTCACTCCAGATCAGCCCAAACTCTCATTT 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
|||||
151 TATGTGTCAGCCAGTCGAGCCTCGGGGGTCCCGACGATTTCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
|||||
201 CAGGCTGTCACACAGCAGCTGACCATCAGCTCGCTCCAGGCTGAGG 250
84 sPGLAAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAl 100
|||||
251 ACGAGCGCGATTATTTACTGTGATCTTTATGACAGCAGTAGCAGTGTCT 300
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
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301 TTCCGCGACGGGACCGAGCTGACGCTCGTGGGT 333
seq_name: gb_om:AF172689
seq_documentation_block:
LOCUS AF172689 333 bp mRNA linear MAM 29-AUG-1999
DEFINITION Ovis aries clone 34 Immunoglobulin light chain variable region
(GLV) mRNA, partial cds.
ACCESSION AF172689
VERSION AF172689.1 GI:5802425
KEYWORDS
SOURCE
ORGANISM
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sheep.
Ovis aries
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 333)
White,G.P., Meusen,E.N.T. and Newton,S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
Unpublished
2 (bases 1 to 333)
White,G.P., Meusen,E.N.T. and Newton,S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
FEATURES
source
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/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="34"
/tissue_type="abomasal lymph node"
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/gene="IGLV"
<1..>333
/gene="IGLV"
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAB51679.1"
/db_xref="GI:5802426"
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SGRLTVLG"
BASE COUNT 68 a 97 c 91 g 77 t
ORIGIN
alignment_scores:
Quality: 445.00 Length: 111
Ratio: 4.450 Gaps: 0

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Percent Similarity: 90.090 Percent Identity: 81.081
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US-09-786-015-4 x AF172689
Align seg 1/1 to: AF172689 from: 1 to: 333
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1 CAGGCTGTGTCAGTACACCGCTCCGCTGTCAGATTCCTCGGGCCAGAG 50
17 gValSerIleThrCysSerGlySerSerSerAsnIleGlyGlnAlaT 34
|||||
51 TGTTCATCACTGCTCTGGAGCAGCAGCAGCATTTGATATGTAATT 100
34 YVVALGTYPTPLTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
|||||
101 ATGTAGTGTGTTCACTCACTCCAGATCAGCCCAAAATCTCTCATTT 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
|||||
151 TATGTGTCAGCCAGTCGAGCCTCGGGGATCCCGACGATTTCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
|||||
201 CAGGCTTGGCACAACAGCAGCTTGTGACCATCAGCTCGCTCCAGGCTGAGG 250
84 sPGLAAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAl 100
|||||
251 ACGAGCTCGGATTATTTACTGTGCTGCTTTATGACAGCAGTAGCAGTGT 300
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
|||||
301 TTCCGCGACGGGACCGAGCTGACGCTCGTGGGT 333
seq_name: gb_om:AF015795
seq_documentation_block:
LOCUS AF015795 333 bp mRNA linear MAM 10-MAR-2000
DEFINITION Bos taurus immunoglobulin light chain variable region mRNA, partial
cds.
ACCESSION AF015795
VERSION AF015795.1 GI:2323379
KEYWORDS
SOURCE
ORGANISM
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cow.
Bos taurus
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 333)
Saini,S.S., Allore,B., Jacobs,R.M. and Kaushtik,A.
Exceptionally long CDR3H region with multiple cysteine residues in
functional bovine IgM antibodies
Eur. J. Immunol. 29 (8), 2420-2426 (1999)
99387993
MEDLINE 10458735
REFERENCE
2 (bases 1 to 333)
Saini,S.S., Jacobs,R. and Kaushtik,A.
Direct Submission
Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph,
ON N1G 2W1, Canada
FEATURES
source
1..333
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BLV48"
/note="bovine x mouse heterohybridoma secreting IgM
antibody"
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/codon_start=1
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/protein_id="AAB6566.1"
/db_xref="GI:2323380"
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GSGTTLFVL"
BASE COUNT 65 a 106 c 94 g 68 t
ORIGIN

alignment_scores:
Quality: 444.50 Length: 111
Ratio: 4.316 Gaps: 1
Percent Similarity: 92.793 Percent Identity: 80.180

alignment_block:
US-09-786-015-4 x AF015795 ..

Align seg 1/1 to: AF015795 from: 1 to: 333

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1 CAGGCTGCTGACTCAGCCGCTCCGCTGCGGGTCCCGGCGCAGAG 50
17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 GGTCTCCATCACCCTGCTGGAACACAGCACCAAGCTGGGCGTGCAT 100
34 yValGlyTPTyTGlnGlnValProGlySerAlaProArgLeuLeuIle 50
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101 ATGGAAGCTGGTCCACACATCCAGAGATCGGCCCCAGAACCTTATC 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TATGCTGCAGACAGTCCAGCCCTGCGGGTCCCGACGATTCCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrIleuThrIleSerSerLeuGlnAlaGlu 84
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CAGGCTGGGAACACAGCACGCTGACCATCAGCTCCGTCAGGCCAGG 250
84 spGluAlaAspTyTyrCysAlaSerTyr...GlnSerThyTyrSerGly 99
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACGAGGCGGATTATTCTGTGCACACTTATGACAGCACTACAAATATGCT 300
100 ValPheGlySerGlyThrArgLeuThrValLeu 110
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seq_name: gb_om:AF015792

seq_documentation_block:

LOCUS AF015792 333 bp mRNA linear MAM 10-MAR-2000
DEFINITION Bos taurus immunoglobulin light chain variable region mRNA, partial
cds

ACCESSION AF015792
VERSION AF015792.1 GI:2323373
KEYWORDS
SOURCE

ORGANISM Bos taurus

cow.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS 1 (bases 1 to 333)
TITLE Salai,S.S., Allore,B., Jacobs,R.M. and Kaushik,A.
JOURNAL Exceptionally long CDR3H region with multiple cysteine residues in
functional bovine IgM antihodles
Eur J Immunol. 29 (8), 2420-2426 (1999)

MEDLINE
PUBMED 99387993
10458755

REFERENCE
AUTHORS 2 (bases 1 to 333)
TITLE Salai,S.S., Jacobs,R. and Kaushik,A.
JOURNAL Direct Submission
Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph,
ON N1G 2W1, Canada

FEATURES
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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="B1V1G9"
/note="bovine x mouse heterohybridoma secreting IgM
antibody"
<1..>333
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAH6563.1"
/db_xref="GI:2323374"
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GSGTTLFVL"

BASE COUNT 66 a 103 c 94 g 70 t
ORIGIN

alignment_scores:
Quality: 443.50 Length: 111
Ratio: 4.306 Gaps: 1
Percent Similarity: 92.793 Percent Identity: 79.279

alignment_block:
US-09-786-015-4 x AF015792 ..

Align seg 1/1 to: AF015792 from: 1 to: 333

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17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 GGTCTCCATCACCCTGCTGGAACACAGCACCAAGCTGGGCGTGCAT 100
34 yValGlyTPTyTGlnGlnValProGlySerAlaProArgLeuLeuIle 50
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 ATGGAAGCTGGTCCACACATCCAGAGATCGGCCCCAGAACCTTAT 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TATGCTGCAGACAGTCCAGCCCTGCGGGTCCCGACGATTTTCGCGCTC 200
67 rArgSerGlyAsnThrAlaThrIleuThrIleSerSerLeuGlnAlaGlu 84
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CAGGCTGGGAACACAGCACACTGACCATCAGCTCCGTCAGGCCAGG 250
84 spGluAlaAspTyTyrCysAlaSerTyr...GlnSerThyTyrSerGly 99
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACGAGGCGGATTATTCTGTGCACACTTATGACAGCACTAGTAATATGCT 300
100 ValPheGlySerGlyThrArgLeuThrValLeu 110
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301 GTTTTCGGCAGCGGACACACATGACCTGACCTGCTC 333
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seq_name: gb_om:AF172684

seq_documentation_block:

LOCUS AF172684 333 bp mRNA linear MAM 29-AUG-1999
DEFINITION Ovis aries clone 17 immunoglobulin light chain variable region
(IGLV) mRNA, partial cds.

ACCESSION AF172684
VERSION AF172684.1 GI:5802415
KEYWORDS
SOURCE

ORGANISM sheep.

Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
AUTHORS 1 (bases 1 to 333)
TITLE White,G.P., Meusen,E.N.T. and Newton,S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal

JOURNAL nematode parasite Haemonchus contortus
 REFERENCE Unpublished
 2 (bases 1 to 333)
 AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Centre
 for Animal Biotechnology, The University of Melbourne, Parkville,
 Melbourne, Victoria 3052, Australia

FEATURES
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 /db_xref="taxon:9940"
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 /codon_start=1
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 /db_xref="GI:5802416"
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 SGRRLVYLG"

BASE COUNT 66 a 95 c 92 g 80 t
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alignment_scores:
 Quality: 442.00 Length: 111
 Ratio: 4.420 Gaps: 0
 Percent Similarity: 90.090 Percent Identity: 80.180

alignment_block:
 US-09-786-015-4 x AF172684 ..

Align seg 1/1 to: AF172684 from: 1 to: 333

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1 CAGGCTGTGCTGACTCAGCGCTCTCCGTCGTCAGAGTCCCGGCGCAAG 50
17 gValSerleThrcySerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 TGTCTCCATCAGCTGCTTGGAGAGCAGCAGCAGCTTGATATGTAATT 100
34 yrValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 ATGTGAGCTGTATCCACACAGTCCAGAGATCAGCCCCCAACTCTCTATT 150
51 SerAlarThrAspArgAlaSerGlyIleProArgPheSerGlySe 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TATGCTGACACAGTCAGCGCTCAGGGGTCCCGCAGCATTTTCGGGCTC 200
67 rArgSerGlyAsnThrAlarThrLeuThrIleSerSerLeuGlnAlaGua 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CAGGTGTGCAACAGCAGCGCTTTCAGCATCAGTCGCTCCAGGCTGAGG 250
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAl 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACGAGGCCGATTTACTGTGATTTTATGACAGCATTAATTATGTTGTTT 300
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
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301 TTTCGGCAGCGGACAGCGCTGACCTCTCGGCT 333
seq_name: gb_cm:AF172686
seq_documentation_block:
LOCUS AF172686 330 bp mRNA linear MAM 29-AUG-1999
DEFINITION Ovis aries clone 14 immunoglobulin light chain variable region
(IGLV) mRNA, partial cds.
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ACCESSION AF172686
 VERSION AF172686.1
 KEYWORDS GI:5802419
 SOURCE
 ORGANISM
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 sheep.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Caprinae; Ovis.

REFERENCE
 1 (bases 1 to 330)
 White,G.P., Meusen,E.N.T. and Newton,S.E.
 TITLE A single-chain variable region immunoglobulin library from the
 abomasal lymph node of sheep infected with the gastrointestinal
 nematode parasite Haemonchus contortus

JOURNAL Unpublished
 2 (bases 1 to 330)
 AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Centre
 for Animal Biotechnology, The University of Melbourne, Parkville,
 Melbourne, Victoria 3052, Australia

FEATURES
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 1..330
 /organism="Ovis aries"
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 /codon_start=1
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 GTRLVYLG"

BASE COUNT 65 a 98 c 90 g 77 t
 ORIGIN

alignment_scores:
 Quality: 441.50 Length: 111
 Ratio: 4.328 Gaps: 1
 Percent Similarity: 91.892 Percent Identity: 81.081

alignment_block:
 US-09-786-015-4 x AF172686 ..

Align seg 1/1 to: AF172686 from: 1 to: 330

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17 gValSerleThrcySerGlySerSerSerAsnIleGlyGlyAsnAlar 34
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51 TGTCTCCATCAGCTGCTTGGAGAGCAGCAGCAGCTTGATATGTAATT 100
34 yrValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
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101 ATGTGAGCTGTATCCACACAGTCCAGAGATCAGCCCCCAACTCTCTATT 150
51 SerAlarThrAspArgAlaSerGlyIleProArgPheSerGlySe 67
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151 TTTGAGCAACAAGTCAGCGCTCGGGGCTCCCGCAGCATTTTCGGGCTC 200
67 rArgSerGlyAsnThrAlarThrLeuThrIleSerSerLeuGlnAlaGua 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CAGGTGTGCAACAGCAGCGCTTTCAGCATCAGTCGCTCCAGGCTGAGG 250
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAl 100
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251 ACGAGCCGATTATTACTTATCTTATGACAGCACT...AGCTTTGTA 297
101 PheGlySerGlyThrArgLeuThrValIleuGly 111
|||||
298 TTCCGCGACCGGACCGACTGACCTCGTGAGT 330

seq_name: gb_com:AF172687

seq_documentation_block:
LOCUS AF172687 330 bp mRNA linear MAM 29-AUG-1999
DEFINITION Ovis aries clone 146 immunoglobulin light chain variable region
(GLV) mRNA, partial cds.
ACCESSION AF172687
VERSION AF172687.1 GI:5802421
KEYWORDS
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 330)
White, C.P., Meusen, E.N.T. and Newton, S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
nematode parasite Haemonchus contortus
JOURNAL Unpublished
2 (bases 1 to 330)
White, C.P., Meusen, E.N.T. and Newton, S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
FEATURES
source
1..330
location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
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1..330
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/db_xref="GI:5802422"
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APKLIFFATSRASGVPDRFSGSRSGNTATLTIGLQADEADYYCSSYSSSFVFGS
GRLTVTLG"
BASE COUNT 65 a 101 c 90 g 74 t
ORIGIN

alignment_scores:
Quality: 441.50 Length: 111
Ratio: 4.328 Gaps: 1
Percent Similarity: 91.892 Percent Identity: 81.081

alignment_block:
US-09-786-015-4 x AF172687 ..

Align seg 1/1 to: AF172687 from: 1 to: 330

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
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1 CAGGCTGTGCTGACTCAGCCGCTCTCGTCCGACGAGTCCCTGGGCGAG 50
17 gvalserIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
|||||
51 TGCTCATCATCCTGCTCTGGAACAGACAGCAAGCTTGATATGATAT 100
34 yrValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuIle 50
|||||
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101 TTGTGACCTGTGTACCAACAGGTCCAGAGATCAGCCCAACATCTCATC 150
51 SerIalThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
|||||
151 TTTCAGCAACAAAGTCAAGCTCGGGGTCCCGACGATTCCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAla 84
|||||
201 CAGCTGTGCGACACACAGCACTGTGACCATCGCTCCCTCAGGCTAGG 250
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
|||||
251 ACGAGCCGATTATTACTTATCTTATGACAGCACT...AGCTTTGTA 297
101 PheGlySerGlyThrArgLeuThrValIleuGly 111
|||||
298 TTCCGCGACCGGACCGACTGACCTCGTGAGT 330

seq_name: gb_com:AF015798

seq_documentation_block:
LOCUS AF015798 333 bp mRNA linear MAM 10-MAR-2000
DEFINITION Bos taurus immunoglobulin light chain variable region mRNA, partial
cds.
ACCESSION AF015798
VERSION AF015798.1 GI:2323385
KEYWORDS
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 333)
Saint, S.S., Allore, B., Jacobs, R.M. and Kaushik, A.
Exceptionally long CDR3H region with multiple cysteine residues in
functional bovine IgM antibodies
Eur. J. Immunol. 29 (8), 2420-2426 (1999)
JOURNAL MEDLINE 99387993
PUBMED 10458755
REFERENCE
2 (bases 1 to 333)
Saint, S.S., Jacobs, R. and Kaushik, A.
Direct Submission
Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph,
ON N1G 2W1, Canada
FEATURES
source
1..333
location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BLV6D10"
/note="bovine x mouse heterohybridoma secreting IgM
antibody"
<1..>333
/product="immunoglobulin light chain variable region"
/protein_id="AAB6569.1"
/db_xref="GI:2323386"
/translation="QAVLTQPSVSRSIGQSVITCGSSSSNVGNGNYSWYQVPGS
APKLIFFATSRASGVPDRFSGSRSGNTATLTIGLQADEADYYCAAYDSSNNAYF
GSGTTLTVL"
BASE COUNT 64 a 106 c 95 g 68 t
ORIGIN

alignment_scores:
Quality: 440.50 Length: 111
Ratio: 4.277 Gaps: 1
Percent Similarity: 92.793 Percent Identity: 79.279

alignment_block:
US-09-786-015-4 x AF015798 ..

Align seg 1/1 to: AF015798 from: 1 to: 333
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[illegible]

FEATURES	source
LOCUS	AF015799
DEFINITION	Bos taurus immunoglobulin light chain variable region mRNA, partial cds.
ACCESSION	AF015799
VERSION	AF015799.1
KEYWORDS	GI:2323387
SOURCE	COW.
ORGANISM	Bos taurus
REFERENCE	Eulatyrol; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
AUTHORS	1 (bases 1 to 333)
TITLE	Saini, S.S., Allore, B., Jacobs, R.M. and Kaushik, A.
JOURNAL	Exceptionally long CDR3H region with multiple cysteine residues in Eur. J. Immunol. 29 (8), 2420-2426 (1999)
MEDLINE	99387993
PUBMED	10458755
REFERENCE	2 (bases 1 to 333)
AUTHORS	Saini, S.S., Jacobs, R. and Kaushik, A.
TITLE	Direct Submission
JOURNAL	Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph, ON N1G 2W1, Canada
FEATURES	Location/Qualifiers
source	1..333
	/organism="Bos taurus"
	/db_xref="taxon:9913"
	/clone="BLV7F8"
	/note="bovine x mouse heterohybridoma secreting IgM antibody"
	<1..>333
	/codon_start=1
	/product="Immunoglobulin light chain variable region"
	/protein_id="AAB6570.1"
	/db_xref="GI:2323388"
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CDS	
BASE COUNT	64 a 105 c 95 g 69 t
ORIGIN	

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alignment_scores:      quality: 440.50      length: 111
                       ratio:    4.277      caps:    1
Percent Similarity:    92.793      Percent Identity: 79.279

alignment_block:
US-09-786-015-4  x AF015799      ..

Align seg 1/1 to: AF015799 from: 1 to: 333

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1  CAGCGCTGCTCACTACGACGCCCTCTCCGTGCCGGGTCCCTGGGCCAGAG 50
17  gValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlat 34
11  |||||
51  GGTCTCCATCACCTGCTCTCGAAGCAGACAGCAACCTTGCGCGGTGCACATT 100
34  yValAlGlyTrpIrryGlnGlnValAlProGlySerAlaProArgLeuLeu 50
11  |||||
101  ATGTGAACGTGTTCCACACAGATCCAGGATGGCCCCAGCAACTCTCAYTC 150
51  SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyIle 67
11  |||||
151  TATGTGGCCACCAAGTCGAGCCCTCTGGGGTCCCCGACCAATCTCCGGCTC 200
67  rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlna 84
11  |||||
201  CAGGTCTGGGAACACAGCCAGCGTCAACATCACTCGCTCCAGGCCGAGG 250
84  SpGlnAlaAspTyrTyrCysAlaSerTyr..GlnSerThrTyrSerGly 99
11  |||||
251  ACGAGCGGATTAATTCTGTGCGACTTATMGACAGCATAGCAATATATCT 300
100  ValPheGlySerGlyTThrArgLeuThrValLeu 110
11  |||||
301  GTTTCGCGAGGGGAGCCACACTCGACCGGTCTCG 333

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```

seq_name: gb_com:AF015801
seq_documentation_block:
LOCUS       AF015801                333 bp    mRNA    linear    MAM 10-MAR-2000
DEFINITION  Bos taurus Immunoglobulin light chain variable region mRNA, partial cds.
ACCESSION   AF015801
VERSION     AF015801.1
KEYWORDS    GI:2323391
SOURCE      .
  ORGANISM  .
            cow.
            Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 333)
AUTHORS    Saini,S.S., Allore,B., Jacobs,R.M. and Kaushik,A.
TITLE      Exceptionally long CDRH region with multiple cysteine residues in
            functional bovine IgM antibodies
JOURNAL     Eur. J. Immunol. 29 (8), 2420-2426 (1999)
MEDLINE    99387993
PUBMED     10458755
REFERENCE   2 (bases 1 to 333)
AUTHORS    Saini,S.S., Jacobs,R. and Kaushik,A.
TITLE      Direct Submission
JOURNAL     Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph,
            ON N1G 2W1, Canada
FEATURES   Location/Qualifiers
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             /organism="Bos taurus"
             /db_xref="taxon:9913"
             /clone="BLV9H3"
             /note="Bovine x mouse heterohybridoma secreting IgM
             antibody"
             <1..>333
             /codon_start=1

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/product="Immunoglobulin light chain variable region"
/protein_id="AAB65572.1"
/db_xref="GI:2323392"
/translation="QAVLTQPSVSGSLGQRVSTCGSSSNVGRGVNFMFOIPGSS
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GSGTTLTVL"
BASE COUNT      64 a      106 c      96 g      67 t
ORIGIN

Alignment_scores:
      Quality: 440.50      Length: 111
      Ratio: 4.277      Gaps: 1
Percent Similarity: 92.793      Percent Identity: 79.279

alignment_block:
US-09-786-015-4 x AF015801 ..

Align seg 1/1 to: AF015801 from: 1 to: 313

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1 CAGCGCTGCTGACTGACCGCTCTCCGTCGGGTCCCTGGGCCAGAG 50
17 gvalSerIleThrCysSerGlySerSerSerAsnIleGlyGlnAlaAr 34
51 GGCTCCATCACCTGCTGTGGAAGCAGCAGCAACGTTGGGCGGCAAT 100
34 yValGlyTrpTrpGlnGlnValProGlySerAlaProArgLeuIle 50
101 ATGTGAACGTGGTCCACACAGATCCCGAGATCGGCCCCAGAACCCATC 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
151 TATGCTGCACCACTGACCTCTGGGGTCCCGACCACTTCTCCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGln 84
201 CAGGTCTGGGAACACAGCCAGCTGACCATCAGCTCCAGGCCAGAG 250
84 sPGLuAlaSPTrpTrpCysAlaSerTyr...GlnSerThrTrpSerGly 99
251 ACGAGCGGATATTCTCTGTGACGCTATGACACAGCATGACAAATATGCT 300
100 valPheGlySerGlyThrArgLeuThrValLeu 110
301 GTTTCGCCAGCGGACACACTGACCGTCCG 333

seq_name: gb_cm:AF172688

seq_documentation_block:
LOCUS AF172688 336 bp mRNA linear MAM 29-AUG-1999
DEFINITION Ovis aries clone 23 immunoglobulin light chain variable region
(ICLV) mRNA, partial cds.
ACCESSION AF172688
VERSION AF172688.1 GI:5802423
KEYWORDS
SOURCE
ORGANISM
sheep.
Ovis aries
Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprine; Ovis.
1 (bases 1 to 336)
white,G.P., Meeusen,E.N.T. and Newton,S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
Unpublished
2 (bases 1 to 336)
white,G.P., Meeusen,E.N.T. and Newton,S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,

```

FEATURES

source	Melbourne, Victoria 3052, Australia Location/Qualifiers 1..336 /organism="Ovis aries" /db_xref="taxon:9940" /clone="23" /tissue_type="abomasal_lymph node" 1..336 /gene="IGLV" <1..>336 /gene="IGLV" /codon_start=1 /product="Immunoglobulin light chain variable region" /protein_id="AAJ51678.1" /db_xref="GI:5802424" /translation="QAVLTDPSSVYRSMGOSVSITCGSSNNVGYNVTWVOOPGS APKLRIKATNRASGVDFRGSRPHRTALTLLTISLDAEDPADVIYCASYDSSTLNLCVF GGSGRLIVLG"
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CDS

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BASE COUNT      68 a       101 c        90 g        77 t
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    Quality:   439.50           Length:     112
    Ratio:     4..351            Gaps:      1
Percent Similarity: 90.179      Percent Identity: 79.464

alignment_block:
US-09-786-015-4 x AFI172688 ...

Align seg 1/1 to: AFI172688 from: 1 to: 336

1 GlnaspValleuthrGlnProSerSerValserGlyLeugIyGlnAr 17
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1 CAGGCCTGTCTGACTCAGCCGTCCTCCGTTACAGTGCCATGCCAGAG 50
17 yvalSerllethrCyseSerGlySerSerSerasnileglyAsnAlat 34
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51 TGTCTCCATCACCTCGCTCTGAAGCAGCAGCAACCTTGATATGTAATT 100
34 y'ValGlyThrpyrrngInvalProGlySerAlaproArgLeuIle 50
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101 ATGTGCACGCGTACCACAGGTCCCAGGATCAGCCCCCAAATTCCTCAT 150
51 SerAlathrThrasparGalaserGlyIleProasParPheserGlySe 67
::::::::::| | | | | | | | | | | | | | | | | | | | |
151 TATGTGCACAACCATGAGCCTCGGGGGTCCCGACCGATT TTCGGCTC 200
67 rArgSerGlyAsnthrlAlathrLeuthrIleSerSerleugInalaGlua 84
||||| ::::::::::| | | | | | | | | | | | | | | | | | |
201 CAGGCCTGCTCCACACAGCAGCTCTGCACATCAGCTCATTCCAGGCTAGAG 250
84 spcLuAlasprtyrryrCysAlasetTyrr...GlnSerThrTryseryg 99
||||| ||||||| | | | | | | | | | | | | | | | | | | |
251 ACGAGGCGCATATTACTGTGCGCTTATGACAGCAGTACTCTTAATGTGT 300
100 ValPheGlySerGlyThrArgLeuthrValalleugly 111
||||| ||||||| | | | | | | | | | | | | | | | | | | |
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seq_name: gb_cm:AFI172693

seq_documentation_block:
LOCUS AFI172693 333 bp mRNA linear MAM 29-AUG-1999
DEFINITION Ovis aries clone 64 immunoglobulin light chain variable region
(GELV) mRNA, partial cds.
ACCESSION AFI172693
VERSION AF172693.1 GI:5802433
KEYWORDS .
SOURCE sheep.
OVIS aries
Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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51 GGTCTCCATCACCCTCTCTGTCGACACAGCAGCATTTGAGGTAATGCTT 100
34 yValGlyTPTrGlnGlnValProGlySerAlaProArgLeuLeu 50
|||||
101 ATGGGGCTGTACCAACAGGTCCAGAGATAGCCCCAGACTCTCTCATTC 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
|||||
151 AGTGCTCAACACCGATCGAGCTCGGGGATCCCGACGATTCCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
|||||
201 CAGTCTGGGAGAACACAGCACCCCTGACCATCAGCTCGCTCAGGCTGAG 250
84 spGluAlaAspTrpTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
|||||
251 ACGAGCGCGATTATTAAGTGTGATCATCAAGTAACTACTTACAGTGTGTT 300
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
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301 TTCGCGACGGGAGACGAGCTGACCGTCTGCGT 333
seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AA158663
seq_documentation_block:
ID AA158663 standard; cDNA; 585 BP.
AC AA158663;
DT 22-OCT-2001 (first entry)
DE Human polynucleotide SEQ ID NO 866.
XX
XX
XX Human: nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
XX WO200153312-A1.
XX
XX PD 26-JUL-2001.
XX
XX PF 26-DEC-2000; 2000MO-US34263.
XX
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX
XX PA (HYSB-) HYSBQ INC.
XX
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX DR MPI; 2001-442253/47.
XX DR P-PSDB; AAM39507.
XX
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX PS Claim 1; SEQ ID NO 866; 10078bp; English.
XX

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AA42213) with nootropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression;
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX SQ Sequence 585 BP; 113 A; 194 C; 156 G; 122 T; 0 other;
XX
XX
XX alignment_scores:
XX Quality: 389.00 Length: 113
XX Ratio: 3.814 Gaps: 1
XX Percent Similarity: 90.265 Percent Identity: 67.257
XX
XX alignment_block:
XX US-09-786-015-4 x AA158663 ..
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XX Align seg 1/1 to: AA158663 from: 1 to: 585
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XX 1 GlnAspValIleThrGlnProSerSerValSerGlySerLeuGlnArg 17
XX |||||
XX 124 CAGTCTGTGTCGACGACGCGCCCTCAGTGTCTGGGGCCCGACGAGAG 173
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XX 17 gValSerIleThrcysSerGlySerSerAsnIleGlyGlyAsnAlaT 34
XX |||||
XX 174 GGTCCATCTCTCTGTCGAGGAGAGCTCCACACTCGGGCAGGATATG 223
XX
XX 34 yValGlyTPTrGlnGlnValProGlySerAlaProArgLeuLeu 50
XX |||||
XX 224 ATGTACACTGTGTACACGACACTCCAGGAGACGCCCAACTCTCTCATC 273
XX
XX 51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
XX |||||
XX 274 TATGTTACACCAATCGGCCCTCAGGGGTCCCTGACCATTCCTGCGTC 323
XX
XX 67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
XX |||||
XX 324 CAGTCTGGCACCTCAGCTCCCTGGCCATCATCGGCTCCAGGCTGAGG 373
XX
XX 84 spGluAlaAspTrpTyrCysAlaSerTyrGlnSerThrTyrSerGly 99
XX |||||
XX 374 ATGAGGCTGATTATTAAGTGTGATGACAGAGCGCTGAGGTCTCT 423
XX
XX 100 ..ValPheGlySerGlyThrArgLeuThrValLeuGly 111
XX |||||
XX 424 GTGTTATTCGGCGGAGGAGCAAGCTGACCTGCTCTGAGGT 462
XX
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XX seq_documentation_block:
XX ID AAC66525 standard; cDNA; 935 BP.
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XX AC AAC66525;
XX
XX DT 15-FEB-2001 (first entry)
XX
XX DE Human immune system associated protein HISP-7 coding sequence.
XX
XX KW Human; immune system associated protein; HISP-7; immune disorder;
XX KW infection; autoimmune disease; cancer; ss.
XX
XX OS Homo sapiens.

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XX  US6135941-A.
PN
XX
XX  24-OCT-2000.
PD
XX
XX  27-MAR-1998; 98US-0049672.
PF
XX
XX  27-MAR-1998; 98US-0049672.
PR
XX
XX  (INCYTE) INCYTE PHARM INC.
PA
XX  Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR:
PI  Hillman JL, Au-Young J;
XX  WPI: 2001-030926/04.
XX  P-PSDB: AAB36209.
DR
XX  New human immune system associated proteins (HISAP) and polynucleotides
PT  encoding the HISAP, useful for diagnosing, treating or preventing
PT  immune or cell proliferative disorders or infections
PS  Claim 3; Column 83-84; 54pp: English.
XX
XX  The present invention provides the coding and protein sequences for a
CC  number of human immune system associated proteins (HISAPs). These can be
CC  used in the diagnosis and treatment of various autoimmune disorders,
CC  infections and cell proliferation diseases. The diseases include AIDS,
CC  adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC  Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC  gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC  erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ  Sequence 935 BP; 216 A; 299 C; 248 G; 172 T; 0 other;

alignment_scores:
Quality: 388.50 Length: 112
Ratio: 3.847 Gaps: 1
Percent Similarity: 90.179 Percent Identity: 67.857

alignment_block:
US-09-786-015-4 x AAC66525 ..

Align seg 1/1 to: AAC66525 from: 1 to: 935

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131 CAGCTGTGCTGACGACGCCGCTCAGTGTGGGCCCCAGGCGAG 180
17 gvalSerIleThrcYserGlySerSerSerAsnIleGlyGlyAsnAlar 34
|||:|||||:|||||:|||||:|||||:|||||:|||||:
181 GGTGCACATCTCCGACACGCGACAGCTCCACATCGGGGACAGTTATG 230
34 yrValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
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231 ATGTACACTGTACACGACCTTCCAGAACAGCCCCAACCTCCTCATC 280
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
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281 TATGGTGTGTGAATCGGCCCTCAGGGGTCCTGACCGATTCTTGCTC 330
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGln 84
|||:|||||:|||||:|||||:|||||:|||||:|||||:
331 CAAGCTGTGGACCTCAGCTCCTCGGCCATCAGTGGGCTCCAGGCTGAG 380
84 spGlnAlaAspTyrTrpCysAlaSerTyrGlnSerThrTyrSerGly 99
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381 ATGAGCGCTGATTATTACTGCCAGTCTATGACACGACCTGAGTGTG 430
100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
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seq_documentation_block:
ID AAS77073 standard; cDNA; 889 BP.
XX
XX  AAS77073;
AC
XX
XX  13-FEB-2002 (first entry)
DT
XX
XX  DNA encoding novel human diagnostic protein #12877.
DE
XX
XX  Human: chromosome mapping; gene mapping; gene therapy; forensic;
KM  food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX  Homo sapiens.
OS
XX
XX  WO200175067-A2.
PN
XX
XX  11-OCT-2001.
PD
XX
XX  30-MAR-2001; 2001WO-US08631.
PF
XX
XX  31-MAR-2000; 2000US-0540217.
PR
XX  23-AUG-2000; 2000US-0649167.
XX
XX  (HYSE-) HYSBO INC.
PA
XX
XX  Drmanac RT, Liu C, Tang YT;
PI
XX
XX  WPI: 2001-639362/73.
XX  P-PSDB; ABG12886.
DR
XX
XX  New isolated polynucleotide and encoded polypeptides, useful in
PT  diagnostics, forensics, gene mapping, identification of mutations
PT  responsible for genetic disorders or other traits and to assess
PT  biodiversity
XX
XX  Claim 1; SEQ ID No 12877; 103pp: English.
XX
XX  The invention relates to isolated polynucleotide (I) and
CC  polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC  and gene mapping, and in recombinant production of (II). The
CC  polynucleotides are also used in diagnostics as expressed sequence tags
CC  for identifying expressed genes. (I) is useful in gene therapy techniques
CC  to restore normal activity of (II) or to treat disease states involving
CC  (II). (II) is useful for generating antibodies against it, detecting or
CC  quantitating a polypeptide in tissue, as molecular weight markers and as
CC  a food supplement. (II) and its binding partners are useful in medical
CC  imaging of sites expressing (II). (I) and (II) are useful for treating
CC  disorders involving aberrant protein expression or biological activity.
CC  The polypeptide and polynucleotide sequences have applications in
CC  diagnostics, forensics, gene mapping, identification of mutations
CC  responsible for genetic disorders or other traits to assess biodiversity
CC  and to produce other types of data and products dependent on DNA and
CC  amino acid sequences. AAS64197-AAS94564 represent novel human
CC  diagnostic coding sequences of the invention.
CC  Note: The sequence data for this patent did not appear in the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp://ipo.int/pub/published_pat_sequences.
XX
SQ  Sequence 889 BP; 200 A; 293 C; 223 G; 173 T; 0 other;

alignment_scores:
Quality: 387.00 Length: 111
Ratio: 3.909 Gaps: 0
Percent Similarity: 89.189 Percent Identity: 65.766

alignment_block:
US-09-786-015-4 x AAS77073 ..

Align seg 1/1 to: AAS77073 from: 1 to: 889
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AC	AAQ2491;
XX	
DJ	31-JUL-1992 (first entry)
DE	
HU	Human U266 lambda gene.
KW	Human myeloma U266 cell line; rearranged lambda gene; Ig;
KM	immunoglobulin light chain; pTAR-7; heavy chain enhancer;
KW	humoral immunity; transgenic mouse; ATCC No. 72003; ds.
OS	Chimeric Homo sapiens.
XX	
FH	Key
FH	Location/Oualifiers
FT	misc.feature
FT	1..8385
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FT	/note="U266-lambda gene"
FT	misc.feature
FT	8386..9071
FT	/tag=b
FT	/note="portion of 95bp XbaI-EcoRI fragment of pTAR-7 contg. mouse H chain enhancer"
PN	WO9204440-A.
XX	
PD	19-MAR-1992.
PF	
PR	27-AUG-1991; 91MO-1006124.
PA	
PT	29-AUG-1990; 90US-0575005.
PI	(HARD) HARVARD COLLEGE.
PP	Vasicek TJ, Leder P;
DR	WPI; 1992-114348/14.
DT	B cell deficient transgenic non-human animals - comprise DNA
TI	encoding the U266 immunoglobulin light chain and an enhancer
TT	region used as models of B cell deficiency

```

PS      | Disclosure, Fig 7: 41np; English.
XX      |
CC      | This sequence is the EcoRI/HindIII fragment of the rearranged lambda
CC      | gene isolated from human myeloma U266 cell line ligated to the mouse
CC      | heavy chain enhancer. The resulting transgene was used in the
CC      | production of transgenic mice in which the proportion of spleen
CC      | cells which are mature B cells is not more than a quarter of that in
CC      | wild-type animals. The animals are more susceptible to infectious
CC      | diseases than the wild-type and are models for severe B cell
CC      | deficiency. See also AA022489 for the transgene sequence.
XX      |
S0      | Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T; 0 other;

alignment_scores:
      Quality: 387.00      Length: 111
      Ratio: 3.909      Gaps: 0
Percent Similarity: 89.189      Percent Identity: 65.766

alignment_block:
US-09-786-015-4 x AA022491 ..

Align seg 1/1 to: AA022491 from: 1 to: 9071

1      glnaSpValLeuThrIngrInProSerServalSerglySerLeuGlyGlnAr 17
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5440  CGNCTGCCCTCGACTGACGCTCCCTCCGCGCGGCTCTTGACACATC 5489

17      gValSerIleThrcysSerglySerSerseraniIeglyGlyAsnAlaAT 34
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5490  AGTCACCTTCCTCCGACGTGAAACGACGATGACATTTGTTATTTAATT 5539

34      yValaGlyTrpTyrgInGlnValProGlySerAlaProArgLeuLeuIle 50
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5540  ANGTCCTCGGTACCGACAAACACCCAGCAAGACCCCAAACTCATGATC 5589

51      SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5590  TATGAGCGACTAAGCGGCCCTCAGGGGCTCCCAACCGCTTCTGCGCTC 5639

67      rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlnA 84
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5640  CAAAGCTGTGCACAAACGGCCCTCCTGACCGCTCTGTGGCTCCAGGCTGAG 5689

84      spGlnAlaAspTyrTyrcysAlaSerTyrgInSerThrTyrsGlyVal 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5690  ATGAGAGCTGATTATTACTGCAGCTCATACGACGACGAGCGATATGTTGATT 5739

101      PheGlySerGlyThrArgLeuThrValIleuGly 111
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
5740  TTCGGCGGAGGACCGAGCTGACCGCTCATTGAGT 5772

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NAI1992.DAT:AA023370
seq_documentation_block:
ID      | AA023370 standard; DNA; 9071 BP.
XX      |
AC      | AA023370:
XX      |
DT      | 14-AUG-1992 (first entry)
XX      |
DE      | U266-Lambda gene and downstream murine Ig Heavy chain enhancer.
XX      |
KW      | Lambda-E-mu; rearranged; immunoglobulin; light chain; transgene;
KW      | B cell deficiency; common variable immunodeficiency; CVID;
KW      | ATCC # 72003; ds.
XX      |
OS      | Chimeric Mus.
OS      | Chimeric Homo sapiens.
XX      |
PN      | W09204443-A.
XX      |

```

PD 19-MAR-1992.
 XX
 PF 27-AUG-1991: 91MO-US06106.
 XX
 PR 29-AUG-1990: 90US-0575006.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Vasilek TJ, Leder P;
 XX
 DR WPI: 1992-114351/14.
 XX
 PT B cell deficient transgenic FVB/N mice - comprise DNA encoding
 PT the lambda light chain of a non-human animal for modelling of B
 PT cell deficiency
 XX
 PS Disclosure: Fig 7; 41pp: English.
 XX
 CC DNA from the Ige-lambda human myeloma U266 cell line was digested
 CC with EcoRI and used to prepare a phage library. The clone
 CC containing the active lambda gene was identified by probing the
 CC library with a radiolabelled BamHI fragment of the human lambda 2
 CC gene. (The complete sequence of U266-lambda gene has EMBL Acc. #
 CC X5154). The lambda-E-mu construct was prepared by cutting the
 CC lambda construct at the HindIII site 0.9kb downstream of
 CC C(lambda)2. The fragment was blunt-ended and ligated to a 955bp
 CC XbaI fragment of pRAR-7 containing the mouse Ig heavy chain
 CC enhancer. The transgene construct was used to transfect mouse
 CC cells for the production of B cell deficient transgenic mice. The
 CC mice can be used to study e.g. X-linked agammaglobulinemia.
 XX
 SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T; 0 other;

alignment_scores:
 Quality: 387.00 Length: 111
 Ratio: 3.909 Gaps: 0
 Percent Similarity: 89.189 Percent Identity: 65.766

alignment_block:

US-09-786-015-4 x AA023370 ..

Align seg 1/1 to: AA023370 from: 1 to: 9071

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5440 CAGCTGCTCCTGACTCAGCTCCTCCCTCGCGTCCGGTCTTGACAGTC 5489
 17 gvalSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaT 34
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5490 AGTCACCTTCTCCTCGACGTGGAACACAGCAGTGCATTTGTAATATAT 5539
 34 yrValGlyTrpTyrgInGlnValProGlySerAlaProArGleuLeuIle 50
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5540 ATGTCTCTCTGCTACCGACACACACACAGCAGCAAGCCCAAACTCATGATC 5589
 51 SerAlaThrhrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5590 TATGAGGTCTACTAAGCGCCCTCAGGGGTCTTAACCGCTTCTTGCTC 5639
 67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGluA 84
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5640 CAAGTCTGGCAACACAGCGCTCCTCGACCGCTCTCGGGCTCCAGGCTACG 5689
 84 spGluAlaAspTyrrTyrrCysAlaSerTyrgInSerThrTyrrSerGlyVal 100
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5690 ATGAGGCTGATTTATTAATCTCAGCTCAACACAGCAGCAATATAGTTGAT 5739
 101 PheGlySerGlyThrArgLeuThrValLeuGly 111
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5740 TTCGGCGGAGGACCAAGCTGACCGTCTAGGT 5772
 seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: AAS03520

seq_documentation_block:
 ID AAS03520 standard; cDNA; 330 BP.
 XX
 AC AAS03520;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE DNA encoding anti-adipocyte monoclonal antibody light chain, FAT 106.
 XX
 KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
 KW heart disease; complementarity determining region; CDR; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200127279-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 11-OCT-2000; 2000MO-GB03900.
 XX
 PR 12-OCT-1999; 99US-0158612.
 XX
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Edwards BM, Main SH, Vaughan TJ;
 XX
 DR WPI: 2001-282031/29.
 XX
 DR P-PADB: AA002620.
 XX
 PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity
 PT related diseases -
 XX
 PS Disclosure: Page 167; 182pp: English.
 XX
 CC AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy
 CC and light chain coding sequences of the invention. The antibodies can be
 CC used in the treatment of obesity and obesity related diseases. The
 CC antibodies can be used to deliver drugs or pro-drugs directly to the fat
 CC mass of an obese patient or the antibody can be used as a therapeutic
 CC itself. Antibodies binding specifically to adipocytes can be used to
 CC activate the immune system to destroy the cells by complement mediated
 CC lysis. The antibodies may be labeled with a detectable label such as
 CC radiolabel, fluorescent or chemical group and used in methods of
 CC diagnosis in human subjects e.g. to determine the presence of adipocyte
 CC antigen on the surface of an adipocyte to detect or determine the
 CC presence or level of adipocytes in a cell or tissue sample. The
 CC antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease.
 XX
 SQ Sequence 330 BP; 69 A; 101 C; 83 G; 77 T; 0 other;

alignment_scores:
 Quality: 386.00 Length: 110
 Ratio: 3.979 Gaps: 0
 Percent Similarity: 88.182 Percent Identity: 65.455

alignment_block:

US-09-786-015-4 x AAS03520 ..

Align seg 1/1 to: AAS03520 from: 1 to: 330

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 1 CAGTCTGTGACTCAGCTCAGCTCCTCGTGTGGTCTCTGACACAGTC 50
 17 gvalSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaT 34
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 51 GATCACCATCTCTGCTGACGTGGAACACAGCAGTGTGTTATTAAT 100

34 yValGIyTPTyrgInglInValProglYSerAlaProArgLeuLeuIle 50
 |||||
 101 ATGTCTCCTGTACCAACAGCAGCCAGCAAGCCCAACATCATGATT 150
 51 SerIaThrThraSPArgAlaSerGIyLeProSPArgPheSerGIySe 67
 :
 151 TATGAGGCAATTAAGCGCCCTCAGGGGTCCCTATGCGCTCTCGGCTC 200
 67 rArgSerGIyAsnThraIaThrLeuThrIleSerSerLeuGlnAlaGUA 84
 |||||
 201 CAAGTCTGGCAACAGCGGCTCCCTGACCGTCTTAAGACTCCAGGCTGAGG 250
 84 sPGlUAAlaSPTyTyrCysAlaSerTyrgInSerThrTyTyrSerGIyVal 100
 |||||
 251 ATGAGGCGTATTATTACTGACGCTCATATGCAACAGCAGTGTGCTT 300
 101 PheGIySerGIyThraPArgLeuThrValLeu 110
 |||||
 301 TTGGCGGAGGAGCCAGCTGACCGTCTTA 330

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH47733

seq_documentation_block:

ID AAH47733 standard; DNA: 339 BP.
 AC AAH47733;
 XX
 XX 30-NOV-2001 (first entry)
 DE Nucleotide sequence of seq id No. 76.
 XX
 XX Gene library: Immunoglobulin; antibody library; human; ds.
 OS Homo sapiens.
 XX
 XX MO200162907-A1.
 PD 30-AUG-2001.
 XX
 XX 22-FEB-2001; 2001MO-JP01298.
 PF
 XX 22-FEB-2000; 2000JP-0050543.
 PR
 XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
 PA
 XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
 PI Okuno Y, Shiraki K;
 XX
 XX WPI; 2001-565420/63.
 DR P-PDB; AAG65369.
 XX
 XX Producing gene libraries and antibody libraries, involves selecting a
 PT light chain that binds to a heavy chain product to produce a functional
 PT formation, and producing a gene library of the light chain variable
 PT regions -
 XX
 XX Examples: p 150; 181pp; Japanese.
 XX
 XX The invention relates to producing gene libraries, comprising
 CC immunoglobulin light and heavy variable region. The method involves
 CC selecting light chain that binds with the heavy chain product to produce
 CC a functional conformation, producing a gene library comprising a
 CC collection of these light chain variable genes, and combining with gene
 CC library of heavy chain variable genes. The method is used for production
 CC of gene and antibody libraries.
 XX
 XX Sequence 339 BP; 67 A; 104 C; 95 G; 73 T; 0 other;

alignment_scores: Quality: 385.00 Length: 113
 Ratio: 3.812 Gaps: 1

Percent Similarity: 89.381 Percent Identity: 67.257

alignment_block:

us-09-786-015-4 x AAH47733 ..

Align seg 1/1 to: AAH47733 from: 1 to: 339

1 GlnaSPValLeuThrGlnProSerSerValSerGIySerLeuGlnArg 17
 |||
 1 CAGGCTGTGCTCAGCTCAGCCCTCCTCAGTGTCTGGGTGCCAGGAGAG 50
 17 gValSerIleThrcYsSerGIySerSerSerAsnIleGIyGlnAlaT 34
 |||||
 51 GGTGACCAATTCCTGACCTGGAGAGAGCTCCACATCGGGGAGGTATG 100
 34 yValGIyTPTyrgInglInValProglYSerAlaProArgLeuLeuIle 50
 |||||
 101 ATGTACTGTGTACAGAGCTTCCAGAGACAGCCCAACATCTCTCATTC 150
 51 SerIaThrThraSPArgAlaSerGIyLeProSPArgPheSerGIySe 67
 :
 151 TATGTAACAGCAATTAAGCGCCCTCAGGGGTCCCTGACCGATCTCTGGCTC 200
 67 rArgSerGIyAsnThraIaThrLeuThrIleSerSerLeuGlnAlaGUA 84
 |||||
 201 CAAGTCTGGCAACAGCGGCTCCCTGACCGTCTTAAGACTCCAGGCTGAGG 250
 84 sPGlUAAlaSPTyTyrCysAlaSerTyrgInSerThrTyTyrSerGIy... 99
 |||||
 251 ATGAGGCGTATTATTACTGACGCTCATATGCAACAGCAGTGTGCTAT 300
 100 ...ValPheGIySerGIyThraPArgLeuThrValLeuGIy 111
 |||||
 301 GTGGTATTCGGCGGAGGAGCCAGCTGACCGTCTTA 339

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAI68765

seq_documentation_block:

ID AAI68765 standard; DNA: 351 BP.
 AC AAI68765;
 XX
 XX 22-JAN-2002 (first entry)
 DE Human autoantibody MICA-6 variable region heavy chain DNA.
 XX
 XX Autoantigen: fusion protein; islet cell antigen; MICA autoantibody;
 KW glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;
 KW polyglutular autoimmune syndrome; autoimmune disorder; IA2; GAD65;
 KW variable region; heavy chain; MICA-6; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX EPI149914-A2.
 PN
 XX 31-OCT-2001.
 PD
 XX 29-MAR-2001; 2001EP-0107702.
 PF
 XX 10-APR-2000; 2000DE-1017782.
 PR 25-MAY-2000; 2000DE-1025840.
 XX
 XX (LABO-) LABOR KOCH MERK GMBH.
 PA
 XX Richter W, Rickert M, Rapp I, Dangel W;
 PI
 XX WPI; 2001-640702/74.
 DR P-PDB; AAG80216.
 XX
 XX New fusion protein, useful for diagnosis of diabetes type I and other
 PT metabolic diseases, is reactive with autoantibodies against both
 PT glutamate decarboxylase and islet cell antigen -
 XX

anilinilaminoloy; hepatoctrophinc; us.

301 GTCTTCGGAGTGGGACCA CGGTCA CCGTGCTTAGGT 336

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH42407

```

seq_documentation_block:
ID   AAH42407 standard; DNA; 333 BP.
XX
AC   AAH42407;
XX
DT   01-OCT-2001 (first entry)
XX
DE   Nucleotide sequence of variable light chain fragment of clone G102.
XX
KW   Antibody; light chain; VL; amyloid protein; blood brain barrier;
KM   endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KM   transferrin receptor; neurological disease; Alzheimer's disease;
KM   prion disease; AIDS-related dementia; epilepsy; brain injury; ss.
XX
OS   Homo sapiens.
XX
PN   WO200144300-A2.
XX
PD   21-JUN-2001.
XX
PF   27-NOV-2000; 2000WO-GB04501.
XX
PR   13-DEC-1999; 99US-0170599.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Webster C, Osbourn J, Ward G, Miller K;
XX
DR   WPI: 2001-398131/42.
XX
P-PSDB; AAG62963.
XX
PT   Mixture or panel of antibodies for selecting specific binding members
PT   that cross the blood brain barrier, for use in delivering different
XX
PT   molecules and treating neurological diseases
XX
PS   Disclosure; Page 106; 109pp; English.
XX
XX
CC   The present sequence encodes an antibody variable light chain (VL)
CC   fragment. The fragment is used to produce a mixture or panel of 5
CC   different specific binding members, each comprising an antibody VH
CC   and/or VL variable domain and capable, when displayed on the surface
CC   of filamentous bacteriophage particles or in the case of a specific
CC   binding member comprising the D5 VH and/or VL variable domain when
CC   bound to human serum amyloid protein, to pass through a mammalian
CC   blood brain barrier (BBB). The panel is useful for the selection of
CC   specific binding members with a desired property such as ability to
CC   cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC   ability to bind areas of inflammation in the brain or BBB breakdown or
CC   ability to bind intracellular adhesion molecules and to bind transferrin
CC   receptor. The antibodies are useful in diagnosis, prophylaxis and
CC   treatment of human or animal body, including neurological diseases, such
CC   as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC   and traumatic brain injury and any diseases involving inflammation
CC   occurring within the brain or central nervous system.
XX
SQ   Sequence 333 BP; 72 A; 99 C; 86 G; 76 T; 0 other;

alignment_scores:
      Quality: 382.00      Length: 111
      Ratio: 3.979        Gaps: 0
Percent Similarity: 86.486 Percent Identity: 64.865

alignment_block:
US-09-786-015-4 x AAH42407
..
Align seg 1/1 to: AAH42407 from: 1 to: 333
1 GlnAspValIeThrGlnProSerSerValSerIysLeuGlyGlnAr 17
||||:|||||:|||||:|||||:|||||:|||||:|||||
1 CAGTCTGTGCTGACATCAGCGCTCCGTCTGTGGTCTCTGGGCACTC 50

```

```

seq_documentation_block:
ID   AAC67868 standard; DNA; 747 BP.
XX
AC   AAC67868;
XX
DT   16-FEB-2001 (first entry)
XX
DE   Recombinant human antibody scFv TN11 nucleotide sequence.
XX
KW   Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
KM   CTN-C; ds.
XX
OS   Homo sapiens.
XX
PN   WO200063699-A1.
XX
PD   26-OCT-2000.
XX
PF   19-APR-2000; 2000WO-EP03550.
XX
PR   20-APR-1999; 99IT-PI00094.
XX
PA   (PHIL-) PHILGEN SRL.
XX
PI   Zardl L;
XX
DR   WPI: 2000-687225/67.
XX
P-PSDB; AAB36083.
XX
PT   Ligands used for diagnosis and treatment of human neoplasias, are
PT   capable of identifying the tenascin-C isoform containing domain C of
XX
PT   tenascin-C -
XX
PS   Claim 8; Page 5-6; 31pp; English.
XX
XX
CC   The present sequence encodes a recombinant human antibody scFv. Antibody
CC   TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope
CC   recognised by TN11 is located inside domain C of TN-C. TN11 is therefore
CC   only capable of recognising TN-C isoforms containing domain C (CTN-C).
CC   TN11 is useful for detecting the presence of TN-C isoforms in vitro or
CC   in vivo for diagnosing pathologies expressing the CTN-C isoforms of TN-C.
CC   It is useful for the preparation of formulations for the treatment of
CC   human neoplasias.
XX
SQ   Sequence 747 BP; 157 A; 197 C; 231 G; 162 T; 0 other;

```


653 ATGAGGCTGATTATTACTGCCAGTTCTATGACACAGCCTGAGTGTGG 702
100 ValPheGlySerGlyThrArgLeuThrValIleuGly 111
|||||
703 GTGTTGCGGAGGAGGACCAAGCTGACCGTGTAGT 738
seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AA503477
seq_documentation_block:
ID AA503477 standard; cDNA; 330 BP.
XX
AC AA503477;
XX
DT 29-APR-2001 (first entry)
XX
DE DNA encoding anti-adipocyte monoclonal antibody light chain, FAT 64.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
XX heart disease; complementarity determining region; CDR; ss.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB03900.
XX
PR 12-OCT-1999; 99US-0158812.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI: 2001-282031/29.
XX
DR P-PSDB: AAU02577.
XX
PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity
XX related diseases -
XX
PS Disclosure: Page 140-141; 182pp; English.
XX
CC AAS03401-AA503535 represent anti-adipocyte monoclonal antibody heavy
CC and light chain coding sequences of the invention. The antibodies can be
CC used in the treatment of obesity and obesity related diseases. The
CC antibodies can be used to deliver drugs or pro-drugs directly to the fat
CC mass of an obese patient or the antibody can be used as a therapeutic
CC itself. Antibodies binding specifically to adipocytes can be used to
CC activate the immune system to destroy the cells by complement mediated
CC lysis. The antibodies may be labeled with a detectable label such as
CC radiolabel, fluorescent or chemical group and used in methods of
CC diagnosis in human subjects e.g. to determine the presence of adipocyte
CC antigen on the surface of an adipocyte to detect or determine the
CC presence or level of adipocytes in a cell or tissue sample. The
CC antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.
XX
SQ Sequence 330 BP; 70 A; 102 C; 82 G; 76 T; 0 other;
alignment_scores:
Quality: 381.00 Length: 110
Ratio: 3.928 Gaps: 0
Percent Similarity: 88.182 Percent Identity: 64.545
alignment_block:
US-09-786-015-4 x AA503477 ..
Align seg 1/1 to: AA503477 from: 1 to: 330

1 GlnAspValIleuThrGlnProSerSerValSerGlySerIleuGlyGlnAr 17
|||||
1 CAGTCTGTCGTCAGCTGACCTGCTCCGTGTCGTGGCCTCCTGGACAGTC 50
17 gValSerIleuThrGlySerSerGlySerSerAsnIleGlyIleValAsnAr 34
|||||
51 AGTCACCATCTCTGTCACCTGACACGACGACGACATGATGATTAAT 100
34 yValGlyIleuThrGlnValProGlySerAlaProArgIleuIle 50
|||||
101 ATGTCCTCCTGTACCAACACACCCAGCGAGAGCCCAACCTATGATTT 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
:::|
151 TATGAGCTGACTAAGCGCCCTCAGGGGTCCCTGATGCTCTGCTGCTC 200
67 rArgSerGlyAspThrAlaThrIleThrIleSerSerIleuIleAlaGua 84
|::|
201 CAACTCTGGCAACAGCGCTCTCAGCCGTCCTGCGCTCCAGGCTGAGG 250
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
|||||
251 ATGAGGCTGATTATTACTGCAGCTCATATGACAGCAGCAGACACTGTAAT 300
101 PheGlySerGlyThrArgLeuThrValIleu 110
|||||
301 TTCGCGGAGGAGGACCAAGTCCACCGCTCCTA 330
seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH42401
seq_documentation_block:
ID AAH42401 standard; DNA; 333 BP.
XX
AC AAH42401;
XX
DT 01-OCT-2001 (first entry)
XX
DE Nucleotide sequence of variable light chain fragment of clone G93.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
XX endothelial cell; brain cell antigen; inflammation; adhesion molecule;
XX transferrin receptor; neurological disease; Alzheimer's disease;
XX prion disease; AIDS-related dementia; epilepsy; brain injury; ss.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI: 2001-398131/42.
XX
DR P-PSDB: AAG62957.
XX
PT Mixture or panel of antibodies for selecting specific binding members
XX that cross the blood brain barrier, for use in delivering different
XX molecules and treating neurological diseases -
XX
PS Disclosure: Page 103; 109pp; English.
XX
CC The present sequence encodes an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the D5 VH and/or VL variable domain when

CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.

xx
SQ Sequence 333 BP; 71 A; 99 C; 87 G; 76 T; 0 other;

alignment_scores:

Quality:	381.00	Length:	111
Ratio:	3.969	Gaps:	0
Percent Similarity:	86.486	Percent Identity:	64.865

alignment_block:

US-09-786-015-4 x AAH42401 ..

Align seg 1/1 to: AAH42401 from: 1 to: 333

```
1  GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlnAr 17
   |||:::|||||:::|||||:::|||||:::|||||  ||||
1  CAGTCTGTGCTGACTGACCTGCCTCCGTCTGGGCTCTCTGACAGTC 50
   |||:::|||||:::|||||:::|||||:::|||||  ||||
17 gValSerIleThrCysSerGlySerSerSerAsnIleGlyIleAsnAlaT 34
   |||:::|||||:::|||||:::|||||:::|||||  ||||
51 GATCACCATCTCCTGCACTGGAACAGACAGTGTGTATTAAT 100
   |||:::|||||:::|||||:::|||||:::|||||  ||||
34 yValGlyTTPyTyrGlnGlnValProGlySerAlaProArgLeuIle 50
   |||:::|||||:::|||||:::|||||:::|||||  ||||
101 ATGTCCTCTGTACCAACACCAACAGCCCAACCAATCATGATT 150
   |||:::|||||:::|||||:::|||||:::|||||  ||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
   |||:::|||||:::|||||:::|||||:::|||||  ||||
151 TATGAGGGCAGTAAGCGCCCTCAGGGGTTTCTAATGCTTCTGTGCTC 200
   |||:::|||||:::|||||:::|||||:::|||||  ||||
67 PArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
   |||:::|||||:::|||||:::|||||:::|||||  ||||
201 CAAGTCTGGCAACACGCGCTCCTGACAAATCTCGGCTCCAGGCTGAGG 250
   |||:::|||||:::|||||:::|||||:::|||||  ||||
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
   |||:::|||||:::|||||:::|||||:::|||||  ||||
251 ACGAGGCTGATTATTAATGCTGACATATACCAACAGGGGCGACTCGAGTT 300
   |||:::|||||:::|||||:::|||||:::|||||  ||||
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
   |||:::|||||:::|||||:::|||||:::|||||  ||||
301 TTGGCGGAGGAGCAACAGCTGACCTGCTGAGG 333
```

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seq_name: gb_est2:BE476752

```

BASE COUNT      75 a      160 c      123 g      93 t
ORIGIN
alignment_scores:
    Quality: 456.00      Length: 111
    Ratio: 4.427      Gaps: 0
    Percent Similarity: 92.793      Percent Identity: 81.081
alignment_block:

```

```

US-09-786-015-4 x BE476752  ..

Align seq 1/1  to: BE476752  from: 1  to: 451

1  GlnAspValIeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
79  CAGGCGTGTGACTGACTGACGCCGTCTCCGTGTCGGGGTCCCTGGGCGAG 128
17  gValSerIleThrCysSerGlySerSerSerIleGlyGlyAsnAlaT 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
129  GGTCTCCATACCTGCTGCTGGAGACGACGCGCGTGGAAACTGGGCAATT 178
34  y-ValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeuIle 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
179  AAGTGAGCTGTGTTCCACACAGATCCCGAGATCGGGCCCCGAGAACCCCTC 228
51  SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
229  TATGGGCGACCAAGTCGAGCCCTCGGGGGGCCCCCGACCGATTCTCCGGCT 278
67  rArgSerGlyAsnThrAlaThrIleuThrIleSerSerLeuGlnAlaGln 84
||||| ||||||| ||||||| ||||||| ||||||| |||||||
279  CAGGTGTGGGAACACACGCCACCCCTGACCATCACTGCTCCAGGCTGAG 328
84  SpGlnAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
||||| ||||||| ||||||| ||||||| ||||||| |||||||
329  ACGAGGCAAGATTAATTTCTGTGCATCTTATACAGAGTGGTGACACAGCTGT 378
101  pheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||||| ||||||| ||||||| ||||||| |||||||
379  TTGGGCGAGCGGACCAAGCTGACCGTCCGGGT 411

```


Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 83 a 161 c 126 g 97 t

ORIGIN

alignment_scores:

Quality: 444.50 Length: 112

Ratio: 4.358 Gaps: 1

Percent Similarity: 91.071 Percent Identity: 81.250

alignment_block:

US-09-786-015-4 x BE590205 ..

Align seg 1/1 to: BE590205 from: 1 to: 467

```

1 GlnaspValleuthrGlnProSerSerValSerGlySerLeuGlyGlnar 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
74 CAGGCTGCTGACTCAGCCGCTCCTCGCTGCGGAGTCCGCGGCGCAGAG 123
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gvalSerIlethrcysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
124 GGTCTCCATCAGCTGCTGCGCAGCAGCGCAATATGGAAATGGCAATT 173
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 yfValGlyTPTyGlnGlnValProGlySerAlaProArgLeuLeu 50
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 ATGTGAGCTGCTCCACAGATCCAGAGATGCGCCCGCAGCTGCTCTC 223
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 TATAGTGGACACTCGAGCCTGCGGGTCCCGACGATTCGCGGCTC 273
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 fArgSerGlyAsnThrAlaThrIleThrIleSerSerLeuGlnAlaGua 84
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
274 CAGGCTGCGGACACAGCCACTGACTATCAGCTCGCTCAGCGCAGG 323
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThr...TyrSerGly 99
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 ACGAGCGAGATTATTCTGTCATCTCTGACACTAGTAACAGAGAGTGT 373
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 AGATTGCGCAGCGGACACACTGACCTGCTGCTGCTGCTGCTGCTG 409
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

seq_name: gb_est2:BE485669

seq_documentation_block:

LOCUS BE485669 495 bp mRNA linear EST 28-AUG-2000

DEFINITION 172803 BARC 580V Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE485669

VERSION BE485669.1 GI:9605202

KEYWORDS EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
 Unpublished (2000)
 Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 RM 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -m1nscore 18
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACAGTACGACAGC
 Plate: 132 row: F column: 18
 Seq primer: ATTAGGTGACTATAG.
 Location/Qualifiers

FEATURES

source

1..495

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="BARC 580V"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;

Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states."

BASE COUNT 95 a 174 c 131 g 95 t

ORIGIN

alignment_scores:

Quality: 443.00 Length: 111

Ratio: 4.386 Gaps: 0

Percent Similarity: 90.991 Percent Identity: 79.279

alignment_block:

US-09-786-015-4 x BE485669 ..

Align seg 1/1 to: BE485669 from: 1 to: 495

```

1 GlnaspValleuthrGlnProSerSerValSerGlySerLeuGlyGlnar 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
87 CAGGCTGCTGACTCAGCCGCTCCTCGCTGCGGAGTCCGCGGCGCAGAG 136
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gvalSerIlethrcysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 GGTCTCCATCAGCTGCTGCGACAGCAGCAAGCTTGGAACTGGCAATT 186
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 yfValGlyTPTyGlnGlnValProGlySerAlaProArgLeuLeu 50
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
187 TTGTGAGCTGCTCCACAGATCCAGAGATGCGCCCGCAGACCTCTCTC 236
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
237 TATGCTGGACACTCGAGCCTCGGGGTCCCGACGATTCGCGGCTC 286
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 fArgSerGlyAsnThrAlaThrIleThrIleSerSerLeuGlnAlaGua 84
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
287 CAGGCTGCGGACACAGCCACTGACTATCAGCTCGCTCAGCGCTGAGG 336
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThr...TyrSerGlyVal 100
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
337 ACGAGCGAGATTATTCTGTCATCTTGGCAATTTGTAACAAATGCTGT 386
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
387 TTGCGCAGCGGACACACTGACCTGCTGCTGCTGCTGCTGCTGCTG 419
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

seq_name: gb_est2:BE589073

seq_documentation_block:

LOCUS BE589073 564 bp mRNA linear EST 28-AUG-2000

DEFINITION 194817 BARC 580V Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE589073

VERSION BE589073.1 GI:9842112

KEYWORDS EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
 Unpublished (2000)
 Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 RM 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -m1nscore 18
 and -minmatch 12 options.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGC
Plate: 121 row: M column: 18
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source Location/Qualifiers

1..364
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 580Y"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
BASE COUNT 106 a 191 c 155 g 112 t
ORIGIN

alignment_scores:
Quality: 440.00 Length: 111
Ratio: 4.356 Gaps: 0
Percent Similarity: 90.991 Percent Identity: 77.477

alignment_block:

US-09-786-015-4 x BE589073 ..

Align seg 1/1 to: BE589073 from: 1 to: 564

```

1 GlnaspValleuThrGlnProSerSerValSerGlySerleuGlyGlnAr 17
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
100 CAGGCTGTGCTGACACAGCCGCTCTGTCGCGGTCCCTCGGCGCAGAG 149
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gValSerlleThrCysSerGlySerSerSerAnlleGlyGlyAsnAlaT 34
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
150 GATCTCCATCACCTGCTGCTGAGAGCAGCAGCAATGGAAGTGCATTT 199
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 yrvAlGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 ATGTGAGTGTGCTCCACAGATCCAGATGCGCCGCCAGAACCTCATTC 249
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 TACGGTCACACGACATCGACCCAGGGGTCCCGACGATTTCTCCGGCTC 299
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerleuGlnAlaGua 84
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 CAGGCTGTGAGACATAGCCACCTTACCATCAGCTGCTCCAGGCTGAG 349
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAla 100
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350 ACGAGGACGATATTCTGTGTCATCTTANCAAGGTGTAAGACACACTGT 399
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 TTCCGGCGGCGGACATACATTCGCTCTCGGCT 432
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
seq_name: gb_est2:BE476758

```

seq_documentation_block:

LOCUS BE476758 496 bp mRNA linear EST 28-AUG-2000
DEFINITION 160150 BARC 580Y Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE476758
VERSION BE476758.1 GI:9596291
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and Wells, K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGC
Plate: 28 row: L column: 3
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source Location/Qualifiers

1..496
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 580Y"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
BASE COUNT 98 a 167 c 133 g 98 t
ORIGIN

alignment_scores:
Quality: 438.00 Length: 112
Ratio: 4.294 Gaps: 2
Percent Similarity: 91.071 Percent Identity: 80.357

alignment_block:

US-09-786-015-4 x BE476758 ..

Align seg 1/1 to: BE476758 from: 1 to: 496

```

1 GlnaspValleuThrGlnProSerSerValSerGlySerleuGlyGlnAr 17
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
89 CAGGCTGTGCTGACACATCATCCGTCGCGGTCCCTCGGCGCAGAG 138
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gValSerlleThrCysSerGlySerSerSerAnlleGlyGlyAsnAlaT 34
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 GGTCTCCATCACCTGCTGAGAGCAGCAGCAATGTT...GGAATGAT 185
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 yrvAlGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
186 ATGTGAGCTGATCCACACTGATCCAGATGCGCCGCCAGAACCTCATTC 235
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
236 TATGTGACACACATCGACCTCGGGGTCCCGACGATTTCTCGGCTC 285
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerleuGlnAlaGua 84

```

```

|||||
286 CAGGCTGGGAACACAGCCACCTGACCATCAGCTCCAGGCTAGG 335
      84 spgualaasptttrcysalaserlyrgln...SerThTySergly 99
      |||||
      336 ACAGGCGAGTTATTTCTGTGCATCTGCTGAGGTAAGTACGATATGCT 385
      100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
      |||||
      386 GTTTTCGGCAGCGGACACACGTCGCTCGTGGGT 421
seq_name: gb_est2:BG691510

```

```

seq_documentation_block:
LOCUS      BG691510                655 bp    mRNA    linear    EST 02-MAY-2001
DEFINITION 340705 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BG691510
VERSION    BG691510.1  GI:13933330
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 655)
            Sonstegard,T.S., Capucio,A.V., Van Tassel,C.P., Ashwell,M.S. and
            Wells,K.D.
            Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
            Unpublished (2000)
            Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCCGACGACGACG
            Plate: 99 row: 1 column: 6
            Seq primer: ATTAGTGACACTATAG.
            Location/Qualifiers
            source          1..655
                        /organism="Bos taurus"
                        /db_xref="taxon:9913"
                        /clone_lib="BARC 5BOV"
                        /tissue_type="pooled"
                        /lab_host="DH10B"
                        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                        Library made from pooled mRNA isolated from mammary
                        tissues at eight physiological, developmental, and disease
                        states."

```

```

BASE COUNT      129 a      221 c      181 g      124 t
ORIGIN

```

```

alignment_scores:
Quality:      436.50      Length:      112
Ratio:        4.238      Gaps:      1
Percent Similarity: 91.964      Percent Identity: 78.571

```

alignment_block:

US-09-786-015-4 x BG691510 ..

Align seg 1/1 to: BG691510 from: 1 to: 655

```

1 GlnAspValLeuThrGlnProSerSerValSerLeuGlyGlnAr 17
||| |||||
88 CAGGCTGTGCTGACTCAGCCGTCCTCGTGCAGGTCCTCGGCGCAGAG 137

```

```

17 gValSerLleThrcysSerGlySerSerAsnIleGlyGlyAsnAlar 34
|||||
138 GGTCTCCATCACCTGCTGTGAGACAGACGACCAATGTGGAAGTGGCAATT 187
      34 yValAlGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
      |||||
      188 ATGTGAGCTGGTTCACAGATCCAGAGATGGCCCCCAAAATCTCTATTC 237
      51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
      |||||
      238 TATGTGTGACACACTCGAGCCTGTGGGGTCCCGACCATTCCTCGGCTC 287
      67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
      |||||
      288 CAGGCTGGGAACACAGCCACCTGACCATCAGCTCGCTCCAGCCGAGG 337
      84 spgualaasptttrcysalaserlyrgln...SerThTySergly 99
      |||||
      338 ACAGGCGGAGTTATTTCTGTGCATCTCCTGACACTAGTACGAGATT 387
seq_name: gb_est2:BE487574

```

```

seq_documentation_block:
LOCUS      BE487574                493 bp    mRNA    linear    EST 28-AUG-2000
DEFINITION 176397 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE487574
VERSION    BE487574.1  GI:9607107
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 493)
            Sonstegard,T.S., Capucio,A.V., Van Tassel,C.P., Ashwell,M.S. and
            Wells,K.D.
            Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
            Unpublished (2000)
            Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCCGACGACGACG
            Plate: 138 row: 1 column: 11
            Seq primer: ATTAGTGACACTATAG.
            Location/Qualifiers
            source          1..493
                        /organism="Bos taurus"
                        /db_xref="taxon:9913"
                        /clone_lib="BARC 5BOV"
                        /tissue_type="pooled"
                        /lab_host="DH10B"
                        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                        Library made from pooled mRNA isolated from mammary
                        tissues at eight physiological, developmental, and disease
                        states."

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FEATURES

```

source

```

BASE COUNT      95 a      173 c      127 g      98 t
ORIGIN

```

alignment_scores:

Quality: 435.50 Length: 111
Ratio: 4.312 Gaps: 1
Percent Similarity: 90.991 Percent Identity: 77.477

Alignment block:

US-09-786-015-4 x BE487574 ..

Align seg 1/1 to: BE487574 from: 1 to: 493

```
1 GlnaspValleuThrnGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
89 CAGGCTGTGTTGACTCAGCCCTCTCCCTGTCCGGGTCCCTGGGCGAG 138
17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlat 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 AGTCCCATTCACCTGCTCTGGAGACATCATCAGCTCGGAACTGGCAATT 188
34 yrvAlaGlyTTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 ATGTGGCTGTGTTCCACACGATCCAGATCATCCGCCAGAACCTCATG 238
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
239 TATGTGTGACACAGTCAGCCTCGGGGCTCCCGACCATTTCTCGGCTC 288
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
289 TACGCTGTGGAGACACAGCCCTGACCATCATCAGCTCGGAGGCTGAG 338
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAl 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
339 ACGAGCGAGATTATTCTGTGATCTTATCAGAGTGT...AATGCTGT 385
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
386 TTGGCGACGGGAGCCACACTGACGCTCTGGGT 418
```

seq_name: gb_est2:BE483566

seq_documentation_block:

LOCUS BE483566 518 bp mRNA linear EST 28-AUG-2000
DEFINITION 169766 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE483566
VERSION BE483566.1 GI:9603099

KEYWORDS EST.

SOURCE COW.

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and
Wells,K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library

JOURNAL Unpublished (2000)
CONTACT: Sonstegard TS

COMMENT USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414

Email: tads@lpsl.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 23 Row: L Column: 14

Seq primer: ATTTAGTGTGACACTATAG.

Location/Qualifiers
1..518
/organism="Bos taurus"

/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

BASE COUNT 101 a 177 c 141 g 99 t
ORIGIN

alignment_scores:

Quality: 435.00 Length: 112
Ratio: 4.223 Gaps: 2
Percent Similarity: 91.964 Percent Identity: 79.464

alignment_block:

US-09-786-015-4 x BE483566 ..

Align seg 1/1 to: BE483566 from: 1 to: 518

```
1 GlnaspValleuThrnGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
92 CAGGCTGTGTTGACTCAGCCATCATCGTCCGGGTCCCTGGGCGAG 141
17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlat 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
142 GGTCCCATTCACCTGACCGGAGACGACCAATGTT...GGAATGAT 188
34 yrvAlaGlyTTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 ATGTGCTGTGTTCCACACGATCCAGATCATCCGCCAGAACCTCATC 238
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
239 TATGTGTGACACAGTCAGCCTCGGGGCTCCCGACCATTTCTCGGCTC 288
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
289 CAGGCTGTGGAGACACAGCCCTGACCATCATCAGCTCGGAGGCTGAG 338
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSer...Gly 99
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
339 ACGAGCGAGATTATTCTGTGATCTTATCAGAGTGT...AATGCT 388
100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
389 GTTTTGGCAGCGGAGCCACACTGACGCTCTGGGT 424
```

seq_name: gb_est2:BE231054

seq_documentation_block:

LOCUS BE231054 363 bp mRNA linear EST 14-NOV-2000
DEFINITION 253265 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE231054
VERSION BE231054.1 GI:11169668

KEYWORDS EST.

SOURCE COW.

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and
Wells,K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library

JOURNAL Unpublished (2000)
CONTACT: Sonstegard TS

COMMENT USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416


```

:::|||||
390 CTTTTCGGACGGGACACACATGACCTGCTGGGT 425
seq_name: gb_est2:BG689524

seq_documentation_block:
LOCUS BG689524 484 bp mRNA linear EST 02-MAY-2001
DEFINITION 337633 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BG689524
VERSION BG689524.1 GI:13931325
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 484)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAAT
BACKWARD: GTTTCAGTCACGACG
Plate: 102 row: K column: 2
Seq primer: ATTTAGTGACACTATG.
FEATURES
source
1..484
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCWV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 86 a 161 c 136 g 101 t
ORIGIN
alignment_scores:
Quality: 414.00 Length: 111
Ratio: 4.099 Gaps: 0
Percent Similarity: 90.991 Percent Identity: 72.072
alignment_block:
US-09-786-015-4 x BG689524 ..
Align seg 1/1 to: BG689524 from: 1 to: 484
1 GlnAspValLeuThrGlnProSerSerValSerIleuGlnAla 17
||| ||||| ||||| ||||| ||||| ||||| |||||
93 CAGGCTGTACTGACTCAGCCCTCTCCGTCCGCTCCCGGCGCAGAG 142
17 gvalSerIleThrCysSerGlySerSerAsnIleGlyAsnAla 34
||||| ||||| ||||| ||||| ||||| ||||| |||||
143 GGTCCTATCACCCTGCTCTGGAGCAGGACAAATGTTGGCAATG 192
34 yrValGlyTPTrGlnGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| |||||
193 ATGTGAGTTGGTCCACAGATCCAGATGGGCCCAAAATGCTATC 242

```

```

51 SerAlaThrThrsPargAlaSerGlyIleProAspArgPheSerGly 67
:::|||||
243 TATGTCGACACAGACACACCTCTGGGGGTCCCGCAGGATTCGCCGCTC 292
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAla 84
||||| ||||| ||||| ||||| ||||| ||||| |||||
293 CAGGCTGGGAGACACACACCCCTGACCATCAGTCGCTCCAGCGAGG 342
84 spGuaAlaAspTYrTYrCysAlaSerTYrGlnSerThrTYrSerGlyVal 100
||||| ||||| ||||| ||||| ||||| ||||| |||||
343 ACGAGCGGAGATATTATTGTTTCATCTCTCATGATGATGATGATGAT 392
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| |||||
393 TTTCGGCGCGGACACACACTAAGCGTCTGGGT 425
seq_name: gb_est2:BE476453

seq_documentation_block:
LOCUS BE476453 489 bp mRNA linear EST 28-AUG-2000
DEFINITION 159697 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE476453
VERSION BE476453.1 GI:9595986
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 489)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAAT
BACKWARD: GTTTCAGTCACGACG
Plate: 27 row: I column: 22
Seq primer: ATTTAGTGACACTATG.
FEATURES
source
1..489
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCWV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 87 a 174 c 130 g 98 t
ORIGIN
alignment_scores:
Quality: 413.50 Length: 112
Ratio: 4.177 Gaps: 1
Percent Similarity: 88.393 Percent Identity: 75.893
alignment_block:
US-09-786-015-4 x BE476453 ..
Align seg 1/1 to: BE476453 from: 1 to: 489

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```

1  GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
75  CAGTCTGTGTGACTCAGCGCTCTCCGTCTCGGGTCCCTGGGCCAGAG 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  yValSerIleThrCysSerGlySerSerAsnIleGlyGlyAsnAlar 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
125  GGTCTCATCATCCTGCTGTGAGAGCAGCGCTCAGCTGGAGGAGTACAT 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  yValAlaGlyTyrPtyGlnGlnValProGlySerAlaProArgLeuIle 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
175  ATGTGAGCTGTGTCACACAGATCCAGAGTCGGCCCCACAAACCTCATC 224
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
225  TATGTGCGGACGACGAGCGCTCGGGGATCCCGACCGATTCTCCGGCTC 274
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
275  CAGTGGGGGACACAGCCACCTGAGCATGCTCGCTCCAGGCTGAGG 324
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
325  ACGAGCGACGCTACTTGTGTGATCTGCTCAGATCGGCAATGCTGCTGT 374
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  ...PheGlySerGlyThrArgLeuThrValLeuGly 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
375  GCTTTCGGCGCGGACGACTGTGAACGTCTGGGT 410

```

seq_name: gb_est2:BG688615

seq_documentation_block:

LOCUS BG688615 528 bp mRNA linear EST 02-MAY-2001
 DEFINITION 363301 BARC SBOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BG688615
 VERSION BG688615.1 GI:13930416
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 528)
 Sonstegard,T.S., Capucio,A.V., Van Tassel,J.C.P., Ashwell,M.S. and
 Wells,K.D.

REFERENCE
 AUTHORS Mapping of Expressed Sequence Tags from a normalized bovine mammary
 gland cDNA library
 Unpublished (2000)
 Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov

TITLE
 JOURNAL Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mismatch 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTACGACG
 Plate: 104 row: L column: 2
 Seq primer: ATTGAGTACACTATAG.

FEATURES
 source Location/Qualifiers
 1..528

/organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BARC SBOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

BASE COUNT 102 a 187 c 139 g 100 t
 ORIGIN

alignment_scores:
 Quality: 413.50 Length: 111
 Ratio: 4.177 Gaps: 1
 Percent Similarity: 89.189 Percent Identity: 73.874

alignment_block:
 us-09-786-015-4 x BG688615 ..

Align seg 1/1 to: BG688615 from: 1 to: 528

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1  GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
90  CAGCTGTGTGACTCAGCGCTCTCCGTCTCGGGTCCCTGGGCCAGAG 139
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  yValSerIleThrCysSerGlySerSerAsnIleGlyGlyAsnAlar 34
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
140  GGTCTCATCATCCTGCTGTGAGAGCAGCGCTCAGCTGGAGGAGTACAT 186
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  yValAlaGlyTyrPtyGlnGlnValProGlySerAlaProArgLeuIle 50
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
187  ATGTGAGCTGTGTCACACAGATCCAGAGTCGGCCCCACAAACCTCATC 236
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
237  TATGGAGTAGACAGGCGACCGCTCGGGGATCCCGACCGATTCTCCGGCTC 286
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
287  CAGTGGGACACAGCCACCTGAGCATGCTCGCTCCAGGCTGAGG 336
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
337  ACGACGAGTACTTGTGTGATCTGCTCAGATCGGCAATGCTGCTGCTGT 386
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  PheGlySerGlyThrArgLeuThrValLeuGly 111
   ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
387  TTCGGCGCGGACGACTGTGAACGTCTGGGT 419

```

seq_name: gb_est2:BE588329

seq_documentation_block:

LOCUS BE588329 474 bp mRNA linear EST 28-AUG-2000
 DEFINITION 194153 BARC SBOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE588329
 VERSION BE588329.1 GI:9841368
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 474)
 Sonstegard,T.S., Capucio,A.V., Van Tassel,J.C.P., Ashwell,M.S. and
 Wells,K.D.

REFERENCE
 AUTHORS Mapping of Expressed Sequence Tags from a normalized bovine mammary
 gland cDNA library
 Unpublished (2000)
 Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov

TITLE
 JOURNAL Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mismatch 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTACGACG

FEATURES
 source Location/Qualifiers
 1..474

Plate: 115 row: B column: 2
 Seq primer: ATTTCAGTGCACCTATAG.
 Location/Qualifiers

FEATURES

source 1..474
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BARC 5BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORF6; Site_1: XbaI; Site_2: XhoI;
 library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

BASE COUNT 84 a 166 c 129 g 95 t
 ORIGIN

alignment_scores:
 Quality: 413.00 Length: 112
 Ratio: 4.130 Gaps: 2
 Percent Similarity: 89.286 Percent Identity: 76.786

alignment_block:

US-09-786-015-4 x BE588329 ..

Align seg 1/1 to: BE588329 from: 1 to: 474

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1  GlnAspValleuthrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
96  CAGGCTGTGCTGACTCAGCCGCTCCGTCGTCGCGCTCCCTGGGCGCAGAG 145
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
17  gValSerIlethrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaT 34
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
146  GGTCCTCATCACCCTGCTGTGAAAGCAGCAGCAACATC...GGTAGTATA 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34  yrValGlyTPYrYrGlnGlnValProGlySerAlaProArgLeuLeuIle 50
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
193  ATGTGGGCTGTGACCAACAGAGTCCAGAGATCGGCTCAGAACCATCATC 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
51  SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
243  TATGTAGTAGTACAGTCGACCCTCGGGGCTCCCGACCGATTCTCGGCTC 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67  rArgSerGlyAsnThrAlaThrIleuthrIleSerSerLeuGlnAlaGluA 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
293  CAGGCTGGCAACACAGCACACCTGACCATCATGTCCTCCAGGGTGAGG 342
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
84  spGluAlaAspTYrTYrCysAlaSerTYrGlnSerThrTYrSer...Gly 99
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
343  ACGAGGCGAGATATTCTGTGCACTAGTACTTGTAGTGGCAGCGGGGT 392
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
100  ValPheGlySerGlyThrArgLeuThrValLeuGly 111
   ::| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
393  ATTTTCGCGAGCGGCGACCATGACCTGACCGTCTGTGGT 428

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Tue Aug 13 08:57:18 2002

OM of: US-09-786-015-2 to: GenEmbl: * out_format : pfs
Date: Aug 12, 2002 10:39 AM
About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+g2n.model -DEV=xlp
-O=/g2n2.1/USP20.spool/US09786015/runat_12082002.092422_53/app-query.fasta.1.347
-DB=geneml -OPMT=fastap -SUFFIX=p2n.rge -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-DELPO=6.000 -DELEXPT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOR-ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09786015.ecgn1_1.7012 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:
Query: US-09-786-015-2
Query length: 121
Database: GenEmbl: *
Database sequences: 1797656
Database length: 187333701
Search time (sec): 1937.690000

Sequence	Strid	Orig	ZScore	EScore	Len	Documentation
gb.com:AF172663	+	455.50	866.44	6.7e-40	342	AF172663 Ovis aries clone 22.1m
gb.com:AF172660	+	453.00	860.97	1.3e-39	369	AF172660 Ovis aries clone 146.1m
gb.com:AF172662	+	451.00	857.75	2.0e-39	345	AF172662 Ovis aries clone 17.1m
gb.com:OAVRB11G	+	450.50	854.83	3.0e-39	429	249193 O.aries mRNA for immunog
gb.com:BTU55202	+	446.50	846.51	8.6e-39	462	U55202 Bos taurus immunoglobuli
gb.com:OAVR31G	+	444.50	842.86	1.4e-38	453	249161 O.aries mRNA for immunog
gb.com:BTU49773	+	444.00	841.03	1.7e-38	486	U49773 Bos taurus immunoglobuli
gb.com:OAVR211G	+	443.50	841.03	1.7e-38	449	249166 O.aries mRNA for immunog
gb.com:AF172664	+	442.50	840.96	1.7e-38	366	AF172670 Ovis aries clone 57.1m
gb.com:AF172674	+	442.50	840.96	1.7e-38	366	AF172674 Ovis aries clone 92.1m
gb.com:OAVRB151G	+	442.00	838.02	2.5e-38	456	249159 O.aries mRNA for immunog
gb.com:OAVR221G	+	441.00	836.55	3.1e-38	434	249157 O.aries mRNA for immunog
gb.com:BTU49778	+	440.50	834.66	3.9e-38	480	U49778 Bos taurus immunoglobuli
gb.com:AF172659	+	440.00	836.55	3.1e-38	351	AF172659 Ovis aries clone 1.1m
gb.com:OAVRA101G	+	440.00	834.19	4.2e-38	456	249175 O.aries mRNA for immunog
gb.com:OAVRB61G	+	439.00	832.42	5.2e-38	450	249172 O.aries mRNA for immunog
gb.com:OAVRB11G	+	439.00	832.28	5.3e-38	456	249176 O.aries mRNA for immunog
gb.com:AF172660	+	438.50	833.31	4.7e-38	366	AF172660 Ovis aries clone 11.1m
gb.com:OAVR201G	+	438.00	831.40	6.0e-38	452	249165 O.aries mRNA for immunog
gb.com:OAVRA1G	+	438.00	830.33	6.8e-38	456	249170 O.aries mRNA for immunog
gb.com:AF172665	+	437.00	830.66	6.5e-38	357	AF172666 Ovis aries clone 35.1m
gb.com:OAVR111G	+	436.50	827.46	9.9e-38	458	249158 O.aries mRNA for immunog
gb.com:AF172676	+	436.00	828.90	8.2e-38	451	AF172676 Ovis aries clone 100.1m
gb.com:OAVRA191G	+	435.00	826.38	1.1e-37	464	249177 O.aries mRNA for immunog
gb.com:OAVRB11G	+	435.00	824.81	1.4e-37	447	249171 O.aries mRNA for immunog
gb.com:AF097206	+	434.50	823.65	1.6e-37	457	249167 O.aries mRNA for immunog
gb.com:AF172664	+	432.50	821.98	2.0e-37	381	AF097206 Bos taurus clone Bf201
gb.com:AF015498	+	432.00	820.65	2.4e-37	375	AF172664 Ovis aries clone 23.1m
gb.com:OAVRB141G	+	432.00	818.97	2.9e-37	452	249154 Bos taurus immunoglob
gb.com:TRR320201	+	432.00	817.77	3.4e-37	516	AF320201 Tursiops truncatus pat
gb.com:BTU32850	+	431.50	817.58	3.5e-37	474	U32850 Bos taurus clone 16.1m
gb.com:AF015494	+	431.00	816.74	3.0e-37	375	AF015494 Bos taurus immunoglob
gb.com:OAVR121G	+	431.00	816.79	3.8e-37	458	249164 O.aries mRNA for immunog
gb.com:BTJGGHXC	+	429.50	804.79	1.8e-36	1581	X62916 B. taurus mRNA for immun
gb.com:AF172667	+	429.50	816.09	4.2e-37	366	AF172667 Ovis aries clone 47.1m
gb.com:OAVR151G	+	429.00	812.89	6.4e-37	469	249169 O.aries mRNA for immunog
gb.com:AF172679	+	428.50	814.79	5.0e-37	342	AF172679 Ovis aries clone 139.1m
gb.com:AF015499	+	427.50	814.03	5.5e-37	372	AF015499 Bos taurus immunoglob
gb.com:AF172665	+	427.50	812.41	6.8e-37	360	AF172665 Ovis aries clone 34.1m

gb.com:AF172661	+	427.50	812.12	7.1e-37	372	AF172661 Ovis aries clone 14
gb.com:BTU55195	+	427.50	809.59	9.8e-37	492	U55195 Bos taurus immunoglob
gb.com:AF172668	+	427.00	811.38	7.8e-37	363	AF172668 Ovis aries clone 52
gb.com:TRR320196	+	427.00	808.37	1.1e-36	507	A1320196 Tursiops truncatus
gb.com:AF172673	+	426.50	810.81	8.4e-37	348	AF172673 Ovis aries clone 81

seq_name: gb.com:AF172663

seq documentation: 342 bp mRNA linear MAM 01-SEP-1999

LOCUS AF172663
DEFINITION Ovis aries clone 22 immunoglobulin heavy chain precursor (IGHV)

FEATURES

source
1..342
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="22"
/tissue_type="abomasal lymph node"
/note="Isolated from animals infected with Haemonchus contortus"

gene
1..342
/gene="IGHV"
V_region
1..342
/gene="IGHV"
CDS
1..>342
/gene="IGHV"
/codon_start=1
/product="immunoglobulin heavy chain precursor"
/protein_id="AAD52590.1"
/db_xref="GI:5815196"
/translation="OYOLOESGPSLVKPSQSLTCTVSGFSLASYAVNWRQAGKA
LEWGGTSGCYKYYNPKLSLSTRTSKQVSLASVTEDTAAVCYRGIGGI
YWGPELIVTVSS"

BASE COUNT
77 a 103 c 95 g 67 t
ORIGIN

alignment_scores:

Quality: 455.50 Length: 121
Ratio: 4.297 Gaps: 1
Percent Similarity: 87.603 Percent Identity: 74.380

alignment block:

US-09-786-015-2 x AF172663 ..

Align seg 1/1 to: AF172663 from: 1 to: 342

1 GlnValGlnleuGlnGlnGlnSerGlyProSerLeuValYsProSerGlnTh 17
|||||
1 CAGGTGCAACTGCAGAGTGGGAGCCAGCTGTGTAGCCCTCACAGAC 50
|||||
17 rleuSerLeuThCysThrValSerGlyPheSerLeuThLysTyrGly 34
|||||

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51 CCTCTCCCTCACCCTGCACGGCTCTGTGATTCCTCATTTAGCCAGCTATGCTG 100
34 aISerTPValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
101 TTACTGGGTCCGCCAGGCTCCAGGAAAGCAGCTGAGTGGTGTGGTGGC 150
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
151 ATACTGTGTGGTGGATTAATACTATTAACCGGCGCTGAATCCCGGCT 200
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||
201 CAGCATCACCAGGAGCAGCACTCCAGAGCCAGCTCCCTGGCAGCTAGACA 250
84 eValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
|||||
251 GCGTGACAACTGAGACACGCGCGCTACTGTGTAAGAGA..... 294
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
|||||
295 .....TATGGGGCATCTACTGTGGGGCCCGAGACTCTGTGT 329

117 uThrValSerSer 121
|||||
330 CACGCTCTCTCTCA 342

seq_name: gb_om:AF172680
seq_documentation_block:
LOCUS AF172680 369 bp mRNA linear MAM 01-SEP-1999
DEFINITION Ovis aries clone 146 immunoglobulin heavy chain precursor (IGHV)
ACCESSION AF172680
VERSION AF172680.1 GI:5815228
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 369)
White,G.P., Meusen,E.N.T. and Newton,S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
unpublished
2 (bases 1 to 369)
White,G.P., Meusen,E.N.T. and Newton,S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Center
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
Location/Qualifiers
1..369
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="146"
/tissue_type="abomasal lymph node"
/notes="Isolated from animals infected with Haemonchus
contortus"
1..369
/gene="IGHV"
1..369
/gene="IGHV"
<1..>369
/gene="IGHV"
/codon_start=1
/product="immunoglobulin heavy chain precursor"
/protein_id="AAD52606.1"
/db_xref="GI:5815229"
/translatability="OYOLOESGPSILMKPSOTLSTNCSVSGFSITSYSVWVRAPGKA
LEWGAIVSDGASVYNPALKSRLSTRTDTSKSVSLSSVTTEDTAVTYCCARDRFSV
YGHAYLSDIYWGGLLVTS"

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BASE COUNT 78 a 112 c 96 g 83 t
ORIGIN
alignment_scores:
Quality: 453.00 Length: 124
Ratio: 4.118 Gaps: 2
Percent Similarity: 88.710 Percent Identity: 74.194
alignment_block:
US-09-786-015-2 x AF172680 ..
Align seg 1/1 to: AF172680 from: 1 to: 369

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnThr 17
|||||
1 CAGGTGCAACTGAGAGAGTCCGGACCCAGCTGATGAAGCCCTCACAGAC 50
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
51 CCTCTCCCTCACCCTGCCTGCTGTGATTCCTCATTTAGCCAGCTATGCTG 100
34 aISerTPValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
101 TTACTGGGTCCGCCAGGCTCCAGGAAAGCAGCTGAGTGGTGTGGTGGC 150
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
151 ATACTGTGTGGTGGATTAATACTATTAACCGGCGCTGAATCCCGGCT 200
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||
201 CAGGCTCACAGGAGCACTCCAGAGCCAGCTCCCTGGCAGCTAGACA 250
84 eValThrThrGluAspThrAlaIleTyrTyrCysAlaLys..... 97
|||||
251 GCGTGACAACTGAGACACGCGCGCTACTGTGTAAGAGA..... 300
98 SerValAsnGlyAspSerValProTyrGlyLeuAspTyrTrpSerProG 114
|||||
301 AGTGTCTATGTGTCATGCTTAT...CTGTCCATGCATCTACTGTGGGCCAGG 347
114 yLeuLeuLeuThrValSerSer 121
|||||
348 ACTCTGTGTACCGCTCTCTCA 369

seq_name: gb_om:AF172662
seq_documentation_block:
LOCUS AF172662 345 bp mRNA linear MAM 01-SEP-1999
DEFINITION Ovis aries clone 17 immunoglobulin heavy chain precursor (IGHV)
ACCESSION AF172662
VERSION AF172662.1 GI:5815193
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 345)
White,G.P., Meusen,E.N.T. and Newton,S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
unpublished
2 (bases 1 to 345)
White,G.P., Meusen,E.N.T. and Newton,S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Center
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
Location/Qualifiers

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source      1. .345
            /organism="Ovis aries"
            /db_xref="taxon:9940"
            /clone="17"
            /issue_type="abomasal lymph node"
            /note="Isolated from animals infected with Haemonchus
            contortus"
            1. .345
            /gene="IGHV"
            1. .345
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            /gene="IGHV"
            /product="Immunoglobulin heavy chain precursor"
            /protein_id="A052589.1"
            /db_xref="GI:5815194"
            /translation="QVQLQESGPSTLVKPSQTLISLTCTVSGFSLTNYGVGVMDVWVQAQAG
            KALEMIGTIVSGSTFYNNPALKPRLSITRDTKSKQVSLSSVTFEDTAVVYCKRNG
            DYPGGLIVTSS"

BASE COUNT      82 a      102 c      94 g      67 t
ORIGIN

alignment_scores:
    Quality: 451.00      Length: 123
    Ratio: 4.337      Gaps: 3
    Percent Similarity: 84.553      Percent Identity: 76.423

alignment_block:
US-09-786-015-2 x AF172662 ..

Align seg 1/1 to: AF172662 from: 1 to: 345

1 GlnValGlnLeuGlnIuSerGlyProSerLeuValLysProSerGlnTh 17
|||||
1 CAGGTGCAACTGACAGAGTCGGAGCCAGCTGGTGAAGCCCTCACAGAC 50
|||||
17 fLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyr... 32
|||||
51 CCTCTCCCTCACCTGCACAGGCTCTGATCTCATTAACCACTATGGTG 100
|||||
33 .GlyValSerTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeu 48
|||||
101 TTGGTGGAGACTGGGTCCGCCAGGCTCCAGGAAGGCCACTGAGGCTT 150
|||||
49 GlyGlyValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGln 65
|||||
151 GGTAACCATATATAGTGGTGAAGTACATTAACCCGGCCCTGAAACC 200
|||||
65 fArgLeuSerValThrArgAspThrSerLysSerGlnPheSerLeuSerL 82
|||||
201 CCGGCTCAGCATACACAGGACACTACCAAGACCAAGTCTCCCTGTCAT 250
|||||
82 euserSerValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSer 98
|||||
251 TGACACAGGTAAACAACGAGACACGGCCGTGTACTACTG...AAGGA 297
|||||
99 ValAsnGlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLe 115
|||||
298 GGAATATGC.....GACTACTGGGGCCACGAGACT 326
|||||
115 uLeuLeuThrValSerSer 121
|||||
327 CCTGTACACCGTCTCTCA 345

seq_name: gb_om:OAVRB71G

seg documentation block:
LOCUS      OAVRB71G      429 bp      mRNA      linear      MAM 04-FEB-1998
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
(clone VRB7).
ACCESSION 249193

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VERSION      249193.1 GI:794139
KEYWORDS     diversity region; immunoglobulin; immunoglobulin heavy chain;
            joining region; variable region.
SOURCE
ORGANISM     Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Caprinae; Ovis.
REFERENCE    1 (bases 1 to 429)
AUTHORS     Dufour V.
TITLE       Direct Submission
JOURNAL     Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
            1172, IBMIG, 40, avenue du Recteur Plineau, Poitiers, FRANCE, 86022
REPERECES   2 (bases 1 to 429)
AUTHORS     Dufour V. and Nau F.
TITLE       Sheep immunoglobulin mu heavy chain variable region sequence
            unpublished
FEATURES
            location/Qualifiers
            1. .429
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            /db_xref="taxon:9940"
            /clone="VRB7"
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            /rearranged
            1. .429
            /gene="VH"
            1. .>429
            /gene="VH"
            /codon_start=1
            /product="VH region precursor"
            /protein_id="CAA89052.1"
            /db_xref="GI:794140"
            /translation="NKPPLTFLFVLISAPRGVLSQVRLQESGSPSLVPSQTLISLTCTVSG
            FSLTIVAVGWVQAQAGKYPWLGSLISIDGSTYNALSKRLSITRDTKSKQVSLSS
            SVTFEDTAVVYCARRTFSGGFAVGNDIDYWGPGLLIVTSS"

sig_peptide
V_region
D_segment
BASE COUNT      89 a      132 c      117 g      91 t
ORIGIN

alignment_scores:
    Quality: 450.50      Length: 124
    Ratio: 4.095      Gaps: 1
    Percent Similarity: 88.710      Percent Identity: 73.387

alignment_block:
US-09-786-015-2 x OAVRB71G ..

Align seg 1/1 to: OAVRB71G from: 1 to: 429

1 GlnValGlnLeuGlnIuSerGlyProSerLeuValLysProSerGlnTh 17
|||||
58 CAGGTGCGGCTGCAGAGTCCGGAGCCAGCTGGTGAAGCCCTCACAGAC 107
|||||
17 fLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
108 CCTCTCCCTCACCTGCACAGGCTCTGATCTCATTAACCGTCAATGGTG 157
|||||
34 alSerTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGly 50
|||||
158 TAGCGTGGGTCCGCCAGGCTCCAGGAAGGTGCCGAGTGGTGTGTA 207
|||||
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67.
|||||
208 ATAAGCACTGATGAAGACAAAGTCAACCGGCCCTGAATATCCGGCT 257

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67  userValThrArgAspThrSerIysSerGlnPheSerLeuSerLeuSers 84
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
258 CAGCATCACAGGAGGACACCTCCAGAGCCACTCTCCCTGCTACTGAGCA 307
84  erVal1ThrGluAspThrAlaIleTyrTyrCysAlaLys..... 97
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
308 GCGTGCACACTGAGAGACAGCGCGTACTACTGTCAGCAAGAGAACTTTT 357
98  SerValAsnGlyAspSerValProTyrGlyLeuAspTyrTrpSerProG1 114
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
358 AGTGTGTGTGTTGCTGTGGCGATACATCGACTCTGCGGCCAGG 407
114  yLeuLeuLeuThrValSerSer 121
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
408 ACTCTGTGTGTCACCGTCTCTCA 429

seq_name: gb_om:BTU55202

seq_documentation_block:
LOCUS      BTU55202              462 bp      mRNA      linear      MAN 02-MAR-2000
DEFINITION Bos taurus immunoglobulin heavy chain mRNA, variable region,
partial cds, 5' end.
ACCESSION  U55202
VERSION    U55202.1  GI:1335958
KEYWORDS
SOURCE
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovine; Bos.
  1 (bases 1 to 462)
REFERENCE
  AUTHORS   Sinclair,M.C. and Aitken,R.
  TITLE     PCR strategies for isolation of the 5' end of an
            immunoglobulin-encoding bovine cDNA
            Gene 167 (1-2), 285-289 (1995)
  JOURNAL   MEDLINE
            96144289
  AUTHORS   Sinclair,M.C., Glitchist,J. and Aitken,R.
  TITLE     The bovine immunoglobulin repertoire is founded upon
            diversification of a single VH gene family
            unpublished
  JOURNAL   3 (bases 1 to 462)
  AUTHORS   Aitken,R.
  TITLE     Direct Submission
            Submitted (17-APR-1996) R. Aitken, Inst. Biomed. Life Sci, Glasgow
            University, University Avenue, Glasgow G12 8QO, UK
  JOURNAL   Location/Qualifiers
            1..462
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /chromosome="21"
            /map="21q23-24"
            /note="Splenic mRNA; Clone 31"
  V_region  1..57
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            1..>462
            /codon_start=1
            /product="immunoglobulin heavy chain"
            /protein_id="AAB01185.1"
            /gb_xref="GI:1335959"
            /translation="MNPWTLFLVLSAPRGVLSVOLRESGPSVLPQSOTLSITCTVS
            GFSLSYGVGWROAKALECLIGISSGSTRYNALSRSLSTTDNKSQPSLSL
            SVTIEDTATYTCAGGAVASDGRCAVMGSGVSGCCVADMGGLLVTVSSA"
  V_region  58..147
            /note="FR1"
            148..162
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            163..204
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            205..252
            /note="CDR2"
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            /note="FR3"
  V_region

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V_region      349..426
              /note="CDR3"
V_region      427..459
              /note="FR4"
C_region      460..>462
BASE COUNT    86 a      132 c      138 g      106 t
ORIGIN
alignment_scores:
  Quality: 446.50      Length: 134
  Ratio: 4.059
  Percent Similarity: 82.090      Percent Identity: 70.149
alignment_block:
US-09-786-015-2 x BTU55202
Align seg 1/1 to: BTU55202 from: 1 to: 462
1  GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
58  CAGGTGCAGCTGCGGAGCTCGGGCCCGCAGCCTGGTGGAAGCCCTACAGAC 107
17  rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrIysTyrGly 34
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
108 CCTCTCCCTCACCTGCACGCTCTGTGATCTCATTTAGACAGCATATGGTG 157
34  aLseTrPValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGly 50
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
158 TAGCGTGGGTCCGCCAGGCTCCAGGAAAGCGCTGGAGTGTCTGTGCTGT 207
51  ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
208 ATAAGTACTGTGTGCAAGCACACCTATATACAGCCCTCGAATCCCGGCT 257
67  userValThrArgAspThrSerIysSerGlnPheSerLeuSerLeuSers 84
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
258 CAGCATCACAGGAGACACCTCCAGAGCCACTCTCTGCTGCTGACAGCA 307
84  erVal1ThrGluAspThrAlaIleTyrTyrCysAlaLys..... 97
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
308 GCGTGCACATGAGAGACAGCGCCACATACTACTGTGCGAAGAGTGTGCT 357
98  ....SerValAsnGlyAspSerValProTyrGly..... 107
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
358 TATGCTACTGATGATGGTGGACGTTGTGCCAAGTGGGTAGTGTGTCTC 407
108 .....LeuAspTyrTrpSerProGlyLeuLeuLeuThrValSers 121
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
408 TGTGTGTGCGTCGATGCGCTGGGGCCAAAGACTCTGTGTACCGCTCTCT 457
121 er 121
||
458 CA 459

seq_name: gb_om:OAVR31G
seq_documentation_block:
LOCUS      OAVR31G              453 bp      mRNA      linear      MAN 04-FEB-1998
DEFINITION O-aries mRNA for immunoglobulin mu heavy chain variable region
(clone VR3).
ACCESSION  Z49161
VERSION    Z49161.1  GI:794111
KEYWORDS   diversity region; immunoglobulin; immunoglobulin heavy chain;
            joining region; variable region.
SOURCE
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Caprinae; Ovis.
  1 (bases 1 to 453)
REFERENCE
  AUTHORS   Dufour,V.
  TITLE     Direct Submission

```

JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
REFERENCE 2 (bases 1 to 453)
AUTHORS Dufour V., Malinge S. and Nau F.
TITLE The sheep Ig variable region repertoire consists of a single VH family
JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
MEDLINE 96310953
FEATURES
source Location/Qualifiers
1..453
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="VR3"
/tissue_type="spleen"
/rearranged
31..453
/gene="VH"
31..>453
/gene="VH"
/product="VH region precursor"
/protein_id="CA89030.1"
/db_xref="GI:794112"
/translation="MNPMLTFLVLSAPRGVLSQVQLQESGPVLPKPSQTLISCTVSGFSLTSNAVGMWRQAPKALEKVGFIYTRGSIYNPAMKSRISITRIDTSKQVSLIS SVTIEDTAVYVCARDSGYGVGCSIDYWGPELVTS"
31..81
/sig_peptide
/gene="VH"
82..453
/gene="VH"
/product="VH region"
379..453
/gene="VH"
/note="D-JH region"
BASE COUNT 95 a 139 c 119 g 100 t
ORIGIN
alignment_scores:
Quality: 444.50 Length: 123
Ratio: 4.116 Gaps: 2
Percent Similarity: 87.805 Percent Identity: 73.171
alignment_block:
US-09-786-015-2 x OAVR3IG ..
Align seg 1/1 to: OAVR3IG from: 1 to: 453
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
88 CAGGTGAGGTGCGAGTGGGAGCCAGCCTGGTGAAGCCCTCACAGAC 137
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrlsTyrgly 34
|||||
138 CCTCTCCCTCACCGCAGCGTCTCTCGATTCTCATTAACGACCAATGCTG 187
34 alserTPvalArgGlnAlaProGlyLysAlaLeuGlnUtrPleuGly 50
|||||
188 TAGCGTGGGCGCCAGGCTCCAGAAAGACACGAGTGGGTTGCTTC 237
51 ValSerSerGlyAlaLeuThrAlaTyraThrAlaLeuGlnSerArgle 67
::: :::
238 ATATATATCTGAGGAGACATATACTATACCCGCCCATGAATCCGGCT 287
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSers 84
|||||
288 CAGATACACAGGAGACACTTAAGACCAAGTCTCCCTGCTACCTGAGACA 337
84 erValThrThrGlnuAspThrAlaLeuTyrcysAlaLysSerValAsn 100
|||||
338 GCGTGACAACTGAGACACGCGCTGCTACTCTGCAAGAGAT...AGT 384
101 GlysAspSerValProTyrgly.....LeuAspTyrrPseProGlyLe 115

|||||
385 GGTATATGCTATGCTATGCTGCTGCATTCAGCATCTGCGGCCAGGACT 434
115 uLeuLeuThrValSerSer 121
|||||
435 CCTGTCCCTGACCTCTCCCTCA 453
seq_name: gb_cm:BTU49773
seq_documentation_block:
LOCUS BTU49773 486 bp mRNA linear MAY 16-AUG-2001
DEFINITION Bos taurus immunoglobulin rearranged heavy chain variable region
mRNA, partial cds.
ACCESSION U49773
VERSION U49773.1 GI:1293591
KEYWORDS
SOURCE
ORGANISM Bos taurus
COW.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 486)
AUTHORS Berens S.J., Wylie D.E. and Lopez O.J.
TITLE Use of a single VH family and long CDR3s in the variable region of cattle Ig heavy chains
JOURNAL Int. Immunol. 9 (1), 189-199 (1997)
MEDLINE 97196871
PUBMED 9043960
REFERENCE 2 (bases 1 to 486)
AUTHORS Berens S.J., Wylie D. and Lopez O.J.
TITLE Direct Submision
JOURNAL Submitted (22-FEB-1996) Osvaldo J. Lopez, Biological Sciences, University of Nebraska, 325 Manter Hall, Lincoln, NE 68588-0118, USA
FEATURES
source Location/Qualifiers
1..486
/organism="Bos taurus"
/db_xref="taxon:9913"
/cell_type="heterohybridoma"
/tissue_type="spleen"
/dev_stage="adult"
<1..>486
/product="immunoglobulin heavy chain variable region"
/protein_id="AA98654.1"
/db_xref="GI:1293592"
/translation="LRUQRLRGVYTLICSKMNPMLTFLVLSAPRGVLSQVQLQESGPVLPKPSQTLISCTVSGFSLTSNAVGMWRQAPKALEKVGFIYTRGSIYNPAMKSRISITRIDTSKQVSLIS SVTIEDTAVYVCARDSGYGVGCSIDYWGPELVTS"
BASE COUNT 104 a 143 c 131 g 108 t
ORIGIN
alignment_scores:
Quality: 444.00 Length: 129
Ratio: 4.111 Gaps: 2
Percent Similarity: 83.721 Percent Identity: 71.318
alignment_block:
US-09-786-015-2 x BTU49773 ..
Align seg 1/1 to: BTU49773 from: 1 to: 486
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
106 CAACTGACGCTGCCGAGATCGGGCCAGCCTGCGAAGCCCTCACAGAC 155
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrlsTyrgly 34
|||||
156 CCTCTCCCTCACCGCAGGATCTGAGTCTCATTTGACGACTATGGTGG 205
34 alserTPvalArgGlnAlaProGlyLysAlaLeuGlnUtrPleuGly 50

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|||||
206 TAACTGGCTCCAGGCTCCAGGAGGCGCTGAGTGCCTGCTGCT 255
51 ValSerSerGlyAlaLeuThrAlaTyrSphrAlaLeuGlnSerArgLe 67
   |||
256 ATAAGCACTGGTGGAAACACAGGCTATACCCAGCCCTGAAATCCGGCT 305
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
   |||
306 CAGCATCCCAAGGACCACTCCAGAGCCAGTCTCTGTCAGTAGACA 355
84 eValThrThrGluAspThrAlaLeuTyrTyrGlySAlaLysSerVala 100
   |||
356 GCGTGACACCTGAGGACACGCGCATCTACTGTGCAAAAAGTTCCTT 405
101 GlyAspSerValProTyrGlyLeuAspTyr..... 110
   |||
406 GGTGGCGT.....TATGTACTGATTTATATACAGACTTACTGCGTTGA 449
111 ....TTPSerProGlyLeuLeuThrValSerSer 121
   |||
450 TGCGTGGGCGCAAGACTCTGTGTCACCGTCTCCTCA 486

seq_name: gb_om:OAVR21IG

seq_documentation_block:
LOCUS OAVR21IG 449 bp mRNA linear MAM 04-FEB-1998
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
(clone VR21).
ACCESSION 249166
VERSION 249166.1 GI:794107
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 449)
REFERENCE
AUTHORS Dufour V.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
1172, ILMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
2 (bases 1 to 449)
REFERENCE
AUTHORS Dufour V., Mallinck-S. and Nau F.
TITLE The sheep Ig variable region repertoire consists of a single VH
family
JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
FEATURES
MEDLINE 96310953
SOURCE
1. .449 Location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="VR21"
/tissue_type="spleen"
/rearranged
39. .449
/gene="VH"
39. .>449
/gene="VH"
/codon_start=1
/product="VH region precursor"
/protein_id="CA89035.1"
/db_xref="GI:794108"
/translation="MNPMTPLFVL SAPRGVLSOVRLOESGPLVPSQTLSTCVS
GSTITVSGVQARQAKALEMIGGIENOCAGYHPLKSRSLSTITDTSKVSLSLS
SVTSEDTAMTYCVKSFPGKTMGPGGLTVVSS"
39. .89
/gene="VH"
90. .449
/gene="VH"
/product="VH region"
387. .449
D_segment

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BASP COUNT 93 a 138 c 123 g 95 t
ORIGIN
alignment_scores:
Quality: 443.50 Length: 121
Ratio: 4.069 Gaps: 2
Percent Similarity: 90.083 Percent Identity: 73.554

alignment_block:
US-09-786-015-2 x OAVR21IG ..
Align seg 1/1 to: OAVR21IG from: 1 to: 449

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
96 CAGGTGCGGCTGCAGAGTGGGACCGCTGTGGAAGCCCTCACAGAC 145
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrTyrGlyV 34
|||||
146 COTCCCTCACTGCACAGGTCTCGGCTTCTCATTAACCACTACAGTG 195
34 aISerTPValArgGlnAlaProGlyLysAlaLeuGlnTyrLeuGly 50
|||||
196 TAGGCTGGTCCGCGCAGCTCCAGGAAAGCGCTGAGTGGCTGTGCTG 245
51 ValSerSerGlyAlaLeuThrAlaTyrSphrAlaLeuGlnSerArgLe 67
|||||
246 ATGAAATGATGATGATGTCAGGCTATCATCAGCCCTTAAGTCCGCT 295
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||
296 CAGCATCCCAAGGACCACTCCAGAGCCAGTCTCTGTCAGTAGACA 345
84 eValThrThrGluAspThrAlaLeuTyrTyrGlySAlaLysSerVala 100
|||||
346 GCGTGACACCTGAGGACACGCGCATCTACTGTGAGAAATTTTTC 395
101 GlyAspSerValProTyrGlyLeuAspTyrTTPSerProGlyLeuLeu 117
|||||
396 GGTGGAATATAC...TGGGCG.....TACTGGGCGCCAGGACTCTTAGT 436
117 uThrValSerSer 121
|||||
437 CACGCTCTCCTCA 449

seq_name: gb_om:AF172670

seq_documentation_block:
LOCUS AF172670 366 bp mRNA linear MAM 01-SEP-1999
DEFINITION Ovis aries clone 57 immunoglobulin heavy chain precursor (IGHV)
mRNA, partial cds.
ACCESSION AF172670
VERSION AF172670.1 GI:5815209
KEYWORDS
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 366)
REFERENCE
AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 366)
White,G.P., Meusen,E.N.T. and Newton,S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Center
for Animal Biotechnology, The University of Melbourne, Parkville,

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FEATURES Melbourne, Victoria 3052, Australia
 Location/Qualifiers
 source 1..366
 /organism="Ovis aries"
 /db_xref="taxon:9940"
 /clone="57"
 /issue_type="abomasal lymph node"
 /note="Isolated from animals infected with Haemonchus contortus"
 gene 1..366
 /gene="IGHV"
 V_region 1..366
 /gene="IGHV"
 CDS <1..>366
 /gene="IGHV"
 /codon_start=1
 /product="Immunoglobulin heavy chain precursor"
 /protein_id="A052597.1"
 /db_xref="GI:5815210"
 /translation="OYOLOESGSLVKPSQTLSTCTVSGSLTYNAVGVNRPAPGKA
 LEWVGAIMSSGMDYNPALKSRIGITRDRSKNVSLSLSTVEDTAIVYYCVARHWIDN
 TYGPATIDWGEELVTVSS"
 BASE COUNT 87 a 107 c 96 g 76 t
 ORIGIN

alignment_scores:
 Quality: 442.50 Length: 122
 Ratio: 4.060 Gaps: 1
 Percent Similarity: 89.344 Percent Identity: 72.131

alignment_block:
 US-09-786-015-2 x AF172670 ..

Align seg 1/1 to: AF172670 from: 1 to: 366

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1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
1 CAGGTGCACACTGCAGAGTGGGACCCGCTGGTGAAGCCCTCACAAC 50
|||||
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
51 CCTCTCCTCCTACCTGCACGCGTCTGTGATTCATTACCAACTATGCTG 100
|||||
34 aLserTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
101 TAGCCTGGGTCGCCAGGCTCCAGAAAGCATGAGTGGGTTGGTCC 150
|||||
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
151 ATATGAGAGTACTGGGAATACAGACTATTAACCCGCCCTGAATCCGCACT 200
|||||
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
|||||
201 CGGCATCACCGAGGACACCTCCAAAGAACACAGGTCCTCCCTGCACGACA 250
|||||
84 eValTrpThrGlnAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
|||||
251 GCGTCACAACTGAGAGACAGCGCGGTACTACTGTGTAAGACATTGGTAT 300
|||||
101 GlysAspSerVal...ProTyrGlyLeuAspTyrTrpSerProGlyLeuLe 116
|||||
301 GATATATCTTATGACCGGCATATATGACACTACGACGAGCCACGAGACTCT 350
|||||
116 uLeuThrValSerSer 121
|||||
351 GGTCAACGCTCTCTCA 366

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seq_name: gb_om:AF172674
 seq_documentation_block: 366 bp mRNA linear MAM 01-SEP-1999
 LOCUS AF172674
 DEFINITION Ovis aries clone 92 immunoglobulin heavy chain precursor (IGHV)

ACCESSION mRNA, partial cds.
 AF172674
 VERSION AF172674.1 GI:5815217
 KEYWORDS
 SOURCE
 ORGANISM
 Ovis aries
 Sheep.
 Bovidae: Caprinae; Ovis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
 Bovidae; Caprinae; Ovis.
 1 (bases 1 to 366)
 White,G.P., Meusen,E.N.T. and Newton,S.E.
 A single-chain variable region immunoglobulin library from the
 abomasal lymph node of sheep infected with the gastrointestinal
 nematode parasite Haemonchus contortus
 JOURNAL
 REFERENCE
 2 (bases 1 to 366)
 White,G.P., Meusen,E.N.T. and Newton,S.E.
 Direct Submission
 Submitted (26-JUL-1999) School of Veterinary Science, The Center
 for Animal Biotechnology, The University of Melbourne, Parkville,
 Melbourne, Victoria 3052, Australia
 FEATURES
 source 1..366
 /organism="Ovis aries"
 /db_xref="taxon:9940"
 /clone="92"
 /issue_type="abomasal lymph node"
 /note="Isolated from animals infected with Haemonchus contortus"
 gene 1..366
 /gene="IGHV"
 V_region 1..366
 /gene="IGHV"
 CDS <1..>366
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 /codon_start=1
 /product="Immunoglobulin heavy chain precursor"
 /protein_id="A052601.1"
 /db_xref="GI:5815218"
 /translation="OYOLOESGSLVKPSQTLSTCTVSGFSLTYNAVGVNRPAPGKY
 PEWLGSISGSGSTRYNALKSRISITRDRSKSVSLSLSTVEDSAVYYCASDIDG
 VWDISYIHVGPDLVTVSS"
 BASE COUNT 80 a 111 c 97 g 78 t
 ORIGIN

alignment_scores:
 Quality: 442.50 Length: 124
 Ratio: 4.097 Gaps: 3
 Percent Similarity: 87.097 Percent Identity: 75.000

alignment_block:
 US-09-786-015-2 x AF172674 ..

Align seg 1/1 to: AF172674 from: 1 to: 366

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1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
1 CAGGTGCACACTGCAGAGTGGGACCCGCTGGTGAAGCCCTCACAAC 50
|||||
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
51 CCTCTCCTCCTACCTGCACGCGTCTGTGATTCATTACCAACTATGCTG 100
|||||
34 aLserTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
101 TACACTGGGTCGCCAGGCTCCAGAAAGTGGCCGAGGCTTGTGAT 150
|||||
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
151 ATCAGCACTGTGTGAAGCACATATATATGCGCGCTGAATCCGCGCT 200
|||||
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84

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gene	/rearranged	39..434		
	/gene="VH"	39..>434		
CDS	/gene="VH"			
	/codon_start=1			
	/product="VH region precursor"			
	/protein_id="CA89026.1"			
	/db_xref="GI:899353"			
	/translation="MDPLMTLLFLPSAPRGVLNQVLOESGPCLVPSQRLSLCTIVS			
	GFSTSGVMNVRQAPKSLSEWGVMSDSTDYKPAALKSRSLITRDTSRSSQVLSLS			
	SVTSEDRFAMYYCAKSYEYMGPLIVYSS"			
sig_peptide	39..89			
	/gene="VH"			
V_region	90..434			
	/gene="VH"			
	/product="VH region"			
D_segment	387..434			
	/gene="VH"			
	/note="D-JH region"			
BASE COUNT	93 a 131 c 116 g		94 t	
ORIGIN				

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  Quality: 441.00
  Ratio: 4.240
  Percent Similarity: 85.950
  Length: 121
  Gaps: 1
  Percent Identity: 72.727
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alignment_block:

US-09-786-015-2 x OAVR22IG .

Align seg 1/1 to: OAVR22IG from: 1 to: 434

[illegible]

seq_name:	gb_cm:BFU49778
seq_documentation_block:	
LOCUS	BFU49778 480 bp mRNA
DEFINITION	Bos taurus immunoglobulin rearranged heavy chain variable region
ACCESSION	U49778

VERSION	049778.1	GI:1293601
KEYWORDS		
SOURCE	COV.	
ORGANISM	Bos taurus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	
AUTHORS	1 (bases 1 to 480)	
TITLE	Berens,S.J., Wylie,D.E. and Lopez,O.J.	
JOURNAL	Use of a single VH family and long CDR3 in the variable region of cattle Ig heavy chains	
MEDLINE	Int. Immunol. 9 (1), 189-199 (1997)	
PUBMED	9043960	
REFERENCE	2 (bases 1 to 480)	
AUTHORS	Berens,S.J., Wylie,D. and Lopez,O.J.	
TITLE	Direct Submission	
JOURNAL	Submitted (22-FEB-1996) Osvaldo J. Lopez, Biological Sciences,	

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/cell_type="heterozybridoma"
/tissue_type="spleen"
/dev_stage="150 day fetus"
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/protein_10

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/translation="WRLGVVTLICSKMNPWLTLLEVLSPRGVLSQVQLRES

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BASE COUNT      100 a      133 c      138 g      108 t      1 others
ORIGIN
"KMSKSKQVSLSSVTPPEPTATYYCAKDQGVYSGTGIVGYS
alignment_scores:
    Quality: 440.50      Length: 128
    Ratio: 4.117      Gaps: 1
Percent Similarity: 83.594      Percent Identity: 70.312
alignment_block:
US-09-786-015-2 x BTU49778  ..
Align seg 1/1 to: BTU49778 from: 1 to: 480
1  GlnValGlnLeuGlnGlnSerGlyProSerLeuValIysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97  CAGGTGACGACGTGGCGGAGTGGCGGCCCGCAGCTGGTGAAGCCCTCACAGAC 146
17  rIeuSerLeuThrCysThrValSerGlyPheSerLeuThrIlyrGly 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
147  CCTCCCTCCACCTGTAGCGTCTGTGATTCATTAGCAGCATATCTCG 196
34  alserTrpValArgGlnIaProGlyIysAlaLeuGlnIuTrpLeuGlyI 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
197  TAAGTGGGTACGACAGGCTCCAGGAAAGCGCTGGAGTGGCTTGAT 246
51  ValSerSerGlyAlaLeuThrAlaTrpAsnThrAlaLeuGlnSerArg 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
247  ATAAACGACTGGTGAAGACAGGCTATATACCCAGCCCTGAATCCCGGCT 296

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67  userValhargaspMrSerIySSerGlnPhesSerIeuSerIeuSers 84
    |||||.....|.....|.....|.....|.....|.....|
297  GAGCTTACCAAGGACCACTCCAAAGCAAGCTCTCTGTGCAETGAGCA 348
    |||||.....|.....|.....|.....|.....|.....|
84  erValThrThrGlnsPThrAlaIleTyrTyrCysAlaIySSerValAsn 100
    |||||.....|.....|.....|.....|.....|.....|
347  GCGTATCACCTGAGAGCACGGCCCATATCTCTCTGTGGAAAGATCGGGG 366
    |||||.....|.....|.....|.....|.....|.....|

```

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101 GLYASpSerValProTygLy.....LeuAspTy 110
    |||
397 GTGATATATAGTGTATGTTATGTTATGATACATACGTCATGC 446
    |||
110 rTTPSerProGlyLeuLeuLeuThrValSerSer 121
    |||
447 CTGGGCGCAAGACTCCTGCTGACCGCTCTCTCA 480
    |||

seq_name: gb_om:AF172659

seq_documentation_block:
LOCUS   AF172659                351 bp    mRNA    linear    MAM 01-SEP-1999
DEFINITION   Ovis aries clone 1 immunoglobulin heavy chain precursor (IGHV)
            mRNA, partial cds.
ACCESSION   AF172659
VERSION     AF172659.1   GI:5815187
KEYWORDS
SOURCE      sheep.
            Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Caprinae; Ovis.
REFERENCE   1 (bases 1 to 351)
AUTHORS    White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE       A single-chain variable region immunoglobulin library from the
            abomasal lymph node of sheep infected with the gastrointestinal
            nematode parasite Haemonchus contortus
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 351)
AUTHORS    White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE       Direct Submission
JOURNAL     Submitted (26-JUL-1999) School of Veterinary Science, The Center
            for Animal Biotechnology, The University of Melbourne, Parkville,
            Melbourne, Victoria 3052, Australia

FEATURES
    source          1..351
                     location/Qualifiers
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    Ratio: 4.151      Gaps: 1
Percent Similarity: 87.603      Percent Identity: 72.727

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1 |||||||||||||||||||||||||||||||||||||||||||||||
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51 CTTCTCCCTCGCGCTGCGAGCGGCTCTGATTTCTCATTAACAGCAATAGTC 100
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34 aLeuTrpValArgGlnAlaProGlyLysAlaLeuGlnTutPleuGlyGly 50
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101 TAGGCTGGCTCCGCCAGCTCCAGGAAAGCTGCCGCGGTGGTGGGT 150
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51 ValSerSerGlyValAlaLeuThrAlaTyAsnThrAlaLeuGlnSerArgLe 67
    |||
151 ATAGTAGAAGTGGGAGACCATATACCCGCGCTGAGTCCGCGCT 200
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67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSers 84
    |||
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    |||
84 eValThrThrGluAspThrAlaLeuTyTrpCysAlaLysSerValAsn 100
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101 GLYASpSerValProTygLyLeuAspTyTrpSerProGlyLeuLeu 117
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298 .....TATGTCACAAATACCGACTACTGGGCGCCAGACTCTGCT 338
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seq_name: gb_om:OAVRA10IG

seq_documentation_block:
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DEFINITION   O. aries mRNA for immunoglobulin mu heavy chain variable region
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ACCESSION   Z49175.1   GI:794118
VERSION     Z49175.1   GI:794118
KEYWORDS    diversity region; immunoglobulin; immunoglobulin heavy chain;
            joining region; variable region.
SOURCE      sheep.
            Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Caprinae; Ovis.
REFERENCE   1 (bases 1 to 456)
AUTHORS    Dufour V.
TITLE       Direct Submission
JOURNAL     Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
            1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
            2 (bases 1 to 456)
AUTHORS    Dufour V., Malinge,S. and Nau,F.
TITLE       The sheep Ig variable region repertoire consists of a single VH
            family
JOURNAL     J. Immunol. 156 (6), 2163-2170 (1996)
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Quality: 440.00 Length: 121
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alignment_block:
US-09-786-015-2 x OAVRA10IG ..

Align seg 1/1 to: OAVRA10IG from: 1 to: 456

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101 GLyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLe 117
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394 AGTAGTGGCGTGTGGTATTACGACTACTGCGGCCAGGACCTACTGTGT 443
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 Date: Aug 12, 2002 10:46 AM

About: Results were produced by the GenCore software, version 4.5.
 Copyright (c) 1993-2000 CompuGen Ltd.

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AC AAA08400;

DT 13-JUL-2000 (first entry)

DE Carcinoembryonic antigen affinity antibody heavy chain variable region.

KW Carcinoembryonic antigen; CEA; sheep; monoclonal antibody;

KW tumour associated antigen; anti-carcinogenic; cytostatic;

OS Ovis sp.

PN WO200012556-A1.

PD 09-MAR-2000.

PF 20-AUG-1999; 99WO-GB02729.

PR 28-AUG-1998; 98GB-0018915.

PA (KSBI-) KS BIOMEDIX LTD.

PI Harrison PJ;

DR WPI: 2000-375618/32.

DR P-PSDB: AAY82528.

PT A new high-affinity monoclonal antibody that is characterized by an

acid-washed enzyme-linked immunosorbent assay for use in cancer therapy

PS Claim 9; Page 13-14; 21pp; English.

XX The present invention describes a high-affinity monoclonal antibody

characterised by an acid-washed enzyme-linked immunosorbent assay (EIA).

The antibody is used in cancer therapy. Association of the new antibody

with an antigen is favoured over dissociation in vivo and they therefore

have longer localisation times at target sites, resulting in a higher

concentration of antibodies localised at the target sites. Targeting the

antibody to a site in vivo is improved. The concentration of antibody

does not need to be too high which reduces side-effects and costs of

therapy. The present sequence encodes the heavy chain variable region

of a monoclonal antibody having affinity for carcinoembryonic antigen

(CEA), a tumour associated antigen, which is used in the exemplification

of the present invention.

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Percent Similarity: 100.000 Percent Identity: 100.000 Gaps: 0

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101 TTAGTTGGGTCCGCGACGCTCCAGAAAGGCGCTTGAGTGGTATGAGTGT 150
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
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151 GTCTCCAGTGTGCTCACTAACAGCCTATTAACACAGCCCTACAGTCCGACT 200
67 uSerValThrArgAspThrSerIleSerGlnPheSerLeuSerLeuSer 84
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84 eValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
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251 GCGTGAAGTGTGAGGACGCGCATTTACTACTGTGCGAAATCTGTCAAT 300
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
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XX 22-OCT-2001 (first entry)
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XX immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
XX T cell; humanised antibody; autoimmune disorder; graft rejection;
XX allergy; heavy chain; ss.
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XX OS Mus musculus.
XX OS Synthetic.
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XX MO200154732-A1.
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XX PD 02-AUG-2001.
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XX PF 26-JAN-2001; 2001WO-US02653.
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XX PR 27-JAN-2000; 2000US-0178473.
XX
XX (GEMT ) GENETICS INST INC.
XX
XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
XX PI O'Hara D, Hinton P, Tsurushita N;
XX
XX MPI: 2001-483195/52.
XX P-PSDB; AAG66523.
XX
XX Novel antibody-toxic group conjugate comprising an antibody that
XX recognizes a molecule expressed only on activated T cells, useful for
XX modulating immune response for treating autoimmune disorder, allergic
XX response
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XX
XX Example 7; Page 118; 123p; English.
PS
XX The invention relates to an antibody-toxic group conjugate comprising
CC an antibody that specifically recognises a molecule expressed only on
CC activated T cells, and a toxic group. The T cell molecule is
CC preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
CC The antibody of the invention is a humanised anti-CTLA4 antibody
CC comprising a sequence of 128 or 142 amino acids fully defined in the
CC specification. The antibody-toxic group conjugate is useful for
CC modulating the immune response in a subject suffering from a disorder
CC or condition such as autoimmune disorder. Immune response to a graft,
CC allergic response or an immune response to a therapeutic protein.
CC The antibody is also useful for research purposes, e.g., in staining
CC and isolating CTLA4-bearing cells. The antibody is also useful for
CC T-cell typing, for isolating specific IL-2 receptor-bearing cells or
CC fragments of the receptor, for vaccine preparation, and for determining
CC the effectiveness of an agent to down-regulate CTLA4 activity. The
CC present sequence encodes the heavy chain of humanised anti-CTLA4
CC antibody.
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XX Quality: 417.00 Length: 123
XX Ratio: 3.971 Gaps: 1
XX Percent Similarity: 85.366 Percent Identity: 66.667
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XX 17 rleuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
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XX 34 a1SerTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
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XX 169 TATATTGGTTCGCGACGCTCCAGAAAGGCTGTGAGTGGCTGGGAGTA 218
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XX 219 ATATGGCTGTGTGTACCAAAATTAATTCGCTCTCATGTCCAGACT 268
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XX 67 uSerValThrArgAspThrSerIleSerGlnPheSerLeuSerLeuSer 84
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XX 269 GACAAATCAGCAAGAGACACATCCCAAGAACCAAGTTCTTAAACTGACA 318
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XX 319 GTGTGACTGACGCGGACACCGCTTACTACTGTGCGCAGAGCCGCCG 368
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XX AC AAH76443;
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XX 22-OCT-2001 (first entry)
 DE Humanised anti-CTLA4 heavy chain cDNA.
 KW Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
 KW immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
 KW T cell; humanised antibody; autoimmune disorder; graft rejection;
 KW allergy; heavy chain; ss.
 OS Homo sapiens.
 OS Mus musculus.
 OS Synthetic.
 FH Key Location/Qualifiers
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 PN 02-AUG-2001.
 PD 26-JAN-2001; 2001WO-US02653.
 XX 27-JAN-2000; 2000US-0178473.
 PR (GEMV) GENETICS INST INC.
 XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
 PI O'Hara D, Hinton P, Tsurushita N;
 XX WPI: 2001-483195/52.
 DR P-PSDB: AAG66523.
 DR
 PT Novel antibody-toxic group conjugate comprising an antibody that
 PT recognizes a molecule expressed only on activated T cells, useful for
 PT modulating immune response for treating autoimmune disorder, allergic
 PT response -
 XX
 PS Example 7; Fig 10; 123pp; English.
 XX
 PS The invention relates to an antibody-toxic group conjugate comprising
 CC an antibody that specifically recognises a molecule expressed only on
 CC activated T cells, and a toxic group. The T cell molecule is
 CC preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
 CC The antibody of the invention is a humanised anti-CTLA4 antibody
 CC comprising a sequence of 128 or 142 amino acids fully defined in the
 CC specification. The antibody-toxic group conjugate is useful for
 CC modulating the immune response in a subject suffering from a disorder
 CC or condition such as autoimmune disorder, immune response to a graft,
 CC allergic response or an immune response to a therapeutic protein.
 CC The antibody is also useful for research purposes, e.g., in staining
 CC and isolating CTLA4-bearing cells. The antibody is also useful for
 CC T cell typing, for isolating specific IL-2 receptor-bearing cells or
 CC fragments of the receptor, for vaccine preparation, and for determining
 CC the effectiveness of an agent to down-regulate CTLA4 activity. The
 CC present sequence encodes the heavy chain of humanised anti-CTLA4
 XX antibody.
 XX Sequence 468 BP; 111 A; 124 C; 116 G; 117 T; 0 other;

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Percent Similarity:    85.366      Percent Identity: 66.667
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US-09-786-015-2 x AAH76443 .
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14 |||||||
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19 ATATGGGCTGTGGTACCACAAATATATTCGGCTCTCATGTCCGACT 223
20 |||||||
21 |||||||
22 uSerValThrArgAspThrIleSerLysSerGlnPheSerLeuSerLys 84
23 |||||||
24 |||||||
25 GACAAATCAGCAAGACACATCCCAAGAACCAAGTTCCCTTAAAACTCAGCA 322
26 |||||||
27 |||||||
28 erValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
29 |||||||
30 |||||||
31 GTGTGATGTGACGCGACACACCGCTCTACTGTGCGCGAGGCCCCCG 372
32 |||||||
33 |||||||
34 GluAspSerValPro....TyrGlyLeuAspTyrTrpSerProGlyLe 115
35 ::::: |||:|||||
36 |||||||
37 CACGCTATGTATGAAGAGAGGCTATGTATGTGACTACTGGGACAAAGAAC 422
38 |||||||
39 |||||||
40 uLeuLeuThrValSerSer 121
41 ||::::|
42 ||::::|
43 CCTAGTCACAGTCTCCCTCA 441

```

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAT90980

```
seq_documentation_block:
ID AAT90980 standard; DNA; 411 BP.
```

AC AAT909

DT 07-JUL-1998 (first entry)

DE Nucleotide sequence of the heavy chain of Hum4TS.22.

KW HuM4TS.22; antibody; platelet derived growth beta receptor; PDGF-R beta
KW inhibition; intimal hyperplasia; vasculature; restenosis; angioplasty;
KW heavy chain; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
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22	22	22
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26	26	26
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31	31	31
32	32	32
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37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
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47	47	47
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49	49	49
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52	52	52
53	53	53
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57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT	product=	Heavy chain of MATS.22"
FT	.mat_peptide	58.411

PN W09737029-A1.

PD 09-OCT-1997.

PF 19-MAR-1997; 97WO-US04198.

PR 22-MAR-1996; 96US-0621751.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Chang CN, Landolfi NF, Martin U;

DR WPI; 1997-503114/46.

XX

PT PDGF BB-induced proliferation of cells expressing the receptor, used

alignment_scores: Quality: 390.50 Length: 121
 Ratio: 3.828 Gaps: 1
Percent Similarity: 84.298 Percent Identity: 61.983

alignment_block:
US-09-786-015-2 x AAT77852 ..

Align seg 1/1 to: AAT77852 from: 1 to: 420

```
1  GlnValGlnLeuGlnGlnUserGlyProSerLeuValIysProSerGlnTh 17
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61  CAGGTGCAGCTGAGAGAGTCAAGAGCTGCGCTGCGCCCTCACAGAG 110
17  rleuSerLeuThrCysThrValSerGlyPheSerLeuThyLysGly 34
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
111 CCGTGCATCACTTGCACTGCTCTGCGTTTCTTAAACCAAGCTATGCTG 160
34  aIserTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGly 50
   || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
161 TACACTGGGTGCGCCAGCCTCCAGGAAGGCTGAGTGGCGTGGAGTA 210
51  ValSerSerGlyAlaLeuThrAlaIleTyraThrAlaLeuGlnSerArg 67
   : : : : : : : : : : : : : : : : : : : : : : : : : :
211 ATATGGGCTGCTGGAAGCATTAATTAATTCGCTCTCATGTCCAGACT 260
67  uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
261 GAGCATCAGCAAGACAACTTCAAGAGCCAAAGTTTCTTAAATAAGACA 310
84  eValThrThrGlnAspThrAlaIleTyrcysAlaLysSerValAsn 100
   || : : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
311 GCTGCAAACTGATGACACAGCCATGACTGACTGTCAGAGCCTAT... 357
101 GlysAspSerValProTyrcylLeuAspTyrrTrpSerProGlyLeuLe 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
358 GGGACTACGTCACATGCTATGACTGCTGCGGTCAAGAACCTCAGT 407
117 uThrValSerSer 121
   : : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
408 CACCGCTCTCTCA 420
```

seq_name: /SIDSI/gcdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA38902

seq_documentation_block:

ID AAA38902 standard; DNA: 357 BP.

AC AAA38902;

DT 29-AUG-2000 (first entry)

DE 260F9 hybridoma VH domain encoding DNA SEQ ID NO:13.

KN Antigen binding site: immunoglobulin; cancer antigen; immunological;

KW antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;

KW specific binding assay; affinity purification; drug targeting;

KW toxin targeting; imaging; genetic; therapeutic; ss.

XX Homo sapiens.

XX US6054561-A.

XX 25-APR-2000.

XX 07-JUN-1995; 95US-0483749.

XX 21-MAR-1986; 86US-0842476.

XX 08-MAY-1988; 88US-0190778.

XX 11-JAN-1985; 84US-0579776.

XX 11-AUG-1994; 94US-0288981.

XX (CHIR) CHIRON CORP.

XX Ring DB:
XX WPI: 2000-338508/29.
XX P-PSDB: AAY90818.

PT Monoclonal antibody capable of binding to human breast cancer antigen
PT useful for affinity purification, drug or toxin targeting, imaging, and
PT treating cancer

XX Disclosure; Fig 7; 57pp; English.

CC The present invention describes a monoclonal antibody (Mab) (I) that
CC binds to a human breast cancer antigen that is also bound by Mab 454C11
CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also
CC described is a hybridoma that produces (I). (I) is useful in specific
CC binding assays, affinity purification, drug or toxin targeting, imaging,
CC and genetic or immunological therapeutics for various cancers. The
CC present sequence encodes a VH domain derived from a 260F9 hybridoma,
CC which is used in the exemplification of the present invention.

XX Sequence 357 BP; 89 A; 89 C; 93 G; 86 T; 0 other;

alignment_scores: Quality: 389.00 Length: 121
 Ratio: 3.814 Gaps: 1
Percent Similarity: 84.298 Percent Identity: 61.983

alignment_block:
US-09-786-015-2 x AAA38902 ..

Align seg 1/1 to: AAA38902 from: 1 to: 357

```
1  GlnValGlnLeuGlnGlnUserGlyProSerLeuValIysProSerGlnTh 17
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1  GAGGTGCAGCTGAGAGAGTCAAGAGCTGCGCTGCGCCCTCACAGAG 50
17  rleuSerLeuThrCysThrValSerGlyPheSerLeuThyLysGly 34
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
51  GCTGTCATCACTTGCACTGCTCTGCGTTTCTTAAACCAACTATGCTG 100
34  aIserTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGly 50
   || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
101 TACACTGGGTGCGCCAGCCTCCAGGAAGGCTCAGAGTGGCTGAGACA 150
51  ValSerSerGlyAlaLeuThrAlaIleTyraThrAlaLeuGlnSerArg 67
   : : : : : : : : : : : : : : : : : : : : : : : : : :
151 ATATGGGCTGCTGGAAGCATTAATTAATTCGCTCTCATGTCCAGACT 200
67  uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
201 GAGCATCAGCAAGACAACTTCAAGAGCCAAAGTTTCTTAAATAAGACG 250
84  eValThrThrGlnAspThrAlaIleTyrcysAlaLysSerValAsn 100
   || : : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
251 TTCTGCAAACTGATGACACAGCCATGACTGACTGCGTCCAGAC....GAC 294
101 GlysAspSerValProTyrcylLeuAspTyrrTrpSerProGlyLeuLe 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
295 GGGGATTACGACTCTTATCTTGGACTGCTGCGGTCAAGAACCTCAGT 344
117 uThrValSerSer 121
   : : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
345 CACCGTCTCTCA 357
```

seq_name: /SIDSI/gcdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA08033

seq_documentation_block:

ID AAA08033 standard; DNA: 840 BP.

AC AAA08033;

XX

DT 19-JUN-2000 (first entry)
XX
DE Antibody fragment scFv TG8-D4 polynucleotide sequence SEQ ID NO:1.
XX
KW Glutenin subunit; wheat; antibody; immunoassay; identification;
XX plant breeding; grain; flour; bread; pasta; ds.
OS Mus musculus.
PN WO200012557-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-AU00690.
XX
PR 28-AUG-1998; 98AU-0005548.
XX
PA (QUAL-) QUALITY WHEAT CRC LTD.
XX
PI Giersch TM, Skerritt JH, Hill AS;
XX
DR WPI; 2000-256593/22.
XX
PT Immunoassay for discriminating high molecular weight glutenin subunits
PT in wheat useful for identifying desired wheat cultivars in plant
PT breeding, involves using monoclonal antibody specific for glutenin
PT subunits -
XX
PS Claim 17; Page 30; 58pp; English.
XX
CC The present invention describes an immunoassay (I) for assessing
CC processing and/or product quality characteristics of grain from a wheat
CC cultivar, by using a monoclonal antibody or fragment specific for one
CC member of high molecular weight glutenin subunit pair (HMW-GS). The
CC method comprises exposing a wheat grain sample to the antibody, under
CC binding conditions, and detecting the binding. The antibody has been
CC raised with a preparation comprising the HMW-GS member in a
CC substantially denatured form. The immunoassay is useful for assessing
CC processing and/or product quality characteristics of grain from a wheat
CC cultivar and for discriminating HMW-GS in wheat grains associated with
CC superior bread and pasta-making qualities, for identifying preferred
CC wheat cultivars in plant breeding. Simple assessment of HMW-GS
CC composition and wheat grain quality can be done from small samples of
CC grain, meal or flour, e.g. 500mg-10g, making it more economical than
CC prior art large scale analysis methods which are very labour intensive.
CC The present sequence encodes a specifically claimed antibody fragment
CC for use in the method of the invention.
XX
SQ Sequence 840 BP; 210 A; 226 C; 227 G; 176 T; 1 other;
XX
alignment_scores:
Quality: 389.00 Length: 121
Ratio: 3.777 Gaps: 0
Percent Similarity: 85.124 Percent Identity: 61.157
XX
alignment_block:
US-09-786-015-2 x AAA08033 ..
XX
Align seg 1/1 to: AAA08033 from: 1 to: 840
XX
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
20 CAGGTCCAACTGCAGAGTCAGGACCTGGCTTACGCCAGCCCTCAGAG 69
|||||
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTrpAlv 34
:|||||
70 CCGTGCATCAGCTGCAGAGTCTGTCTCTCTTCTTAACTAGCTATGTG 119
|||||
34 alserTrpValArgGlnAlaIapProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||
120 TACACTGGTTCGCCAGCTCTCAGGAAAGGTCTGAGAGTGGCTGGAGTG 169

51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArg 67
::: |||||
170 ATATGGGATATATGGAACACAGACTATATATTCAGCTCTCAAAATCAGACT 219
|||||
67 uSerValThrArgAspThrLysSerGlnPheSerLeuSerLeuSers 84
|||||
220 GAGCATCAGCAAGACACATCCCAAGAGCCAAAGTTTCTTAAATAATGACA 269
84 eValThrThrGluAspThrAlaIleTyrTrpCysAlaLysSerValAsn 100
|||||
270 GTCGCAAACTGATGACACAGCCAGCTACTAGTGTGCAAAAGGATCCCC 319
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
|||||
320 TACTATAGAGATTACTATGCTATGACTACTGGGCGCAAGGACACACGGT 369
117 uThrValSerSer 121
370 CACCGTCTCCTCA 382
seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:AAQ45429
seq_documentation_block:
ID AAQ45429.standard; cDNA to mRNA; 405 BP.
XX
AC AAQ45429;
XX
DT 17-NOV-1994 (first entry)
XX
DE KM-603 heavy chain.
XX
KW Monoclonal antibody; Ab; ganglioside GM2; chimera;
KW chimeric antibody; expression vector; heavy; light; chain;
KW hypervariable region; CDR; constant region; hybridoma;
KW Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer; ds.
XX
OS Rat rattus.
XX
FH Key Location/Qualifiers
FT CDS 10..405
FT /*tag= a
FT /note= "excluding stop codon"
FT sig_peptide 10..66
FT /*tag= b
FT /note= "sig_peptide"
FT misc_feature 157..171
FT /*tag= c
FT /note= "hypervariable region 1"
FT misc_feature 214..261
FT /*tag= d
FT /note= "hypervariable region 2"
FT misc_feature 358..369
FT /*tag= e
FT /note= "hypervariable region 3"
XX
PN AU9346181-A.
XX
PD 17-MAR-1994.
XX
PF 07-SEP-1993; 93AU-0046181.
XX
PR 07-SEP-1992; 92JP-0238452.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI HanaI N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
PI Shitara K;
XX
DR WPI; 1994-126857/16.
XX
PT P-PSDB; AAR53331.
XX
PT Humanised antibody specific for ganglioside GM2 - used for
producing a cytotoxic effect on cancers such as melanoma,

PT neuroblastoma and glioma.
XX
PS Disclosure: Page 109; 191pp; English.
XX
CC Chimeric human Ab expression vectors are constructed by inserting
CC the Ab heavy and light chain variable region-encoding CDNA
CC isolated from hybridomas producing a mouse or rat monoclonal Ab
CC reacting with the ganglioside GM2 respectively into an expression
CC vector for use in animal cells which contains the human Ab heavy and
CC light chain constant region-encoding CDNA. The expression vectors
CC are introduced into animal cells and the transformant thus obtained
CC is cultured for the prodn. of a chimeric human Ab reacting with the
CC ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric
CC human Abs will not cause anti-mouse Ig Ab prodn. in the patient's
CC body but show a prolonged blood half-life, with a reduced frequency
CC of adverse effects, so that it can be expected to be superior
CC to mouse monoclonal Abs in the efficacy in the treatment of human
CC cancer, for instance.
CC Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603
CC heavy and light chain sequences are given in AAQ45426-30.
CC CDR regions for use in chimeric Abs are indicated in the
CC Features Table.
XX
SQ Sequence 405 BP; 95 A; 110 C; 103 G; 97 T; 0 other;

alignment_scores:
Quality: 388.50 Length: 121
Ratio: 3.809 Gaps: 1
Percent Similarity: 84.298 Percent Identity: 62.810

alignment_block:
US-09-786-015-2 x AAQ45429 ..

Align seg 1/1 to: AAQ45429 from: 1 to: 405

```
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
67 CAAGTCAGCTGAAGAGGAGTCAGACCTGCTGCTGTCAGCCCTCACAGAC 116
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
117 CCGTCCCTCACCCTGCACCTGCTCTGCGTCTCATTAACACGCTATACTG 166
34 aLseTrPValArGlnAlaProGlyLysAlaLeuGlnUtrPleuGlyGly 50
|||||
167 TAAGCTGGGTTCCGCGACCTCCAGAGAAAGGTCGGAGTGGATTGGACA 216
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgle 67
|||||
217 ATATCAAGCTGTGAAGCACATATTAATTCAGCTCTCAATACGACT 266
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSers 84
|||||
267 GACACATCAGCAGGAGACACCTCCAAAGACCAAGTTTCTTAATAATGAACA 316
84 eValAlaThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
|||||
317 GTCTGCAACTGAAGACACAGCATTCTGTGCCCCCTTCGAGGGG 366
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
|||
367 GCC.....TGGGGCCCAAGAGATCATGCT 389
117 uThrValSerSer 121
|||
390 CACAGTCTCCTCA 402
```

seq_name: /sids1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAx9477

seq_documentation_block:
ID AAx9477 standard; CDNA to mRNA; 405 BP.
XX

AC AAx9477;
XX
XX 04-NOV-1999 (first entry)
XX
XX Antibody heavy chain KM-603.
DE
XX antibody; nucleotide; genomic; hypervariable region;
XX chimeric; light chain; heavy chain; ds.
XX
XX Rattus sp.
OS
XX
XX Key Location/Qualifiers
FH CDS 10..405 /*tag= a
FT CDS /product= "Rat anti-GM2 heavy chain"
FT sig_peptide 10..66 /*tag= b
FT mat_peptide 67..405 /*tag= c
FT
XX
XX US5939532-A.
XX
XX 17-AUG-1999.
XX
XX 07-JUN-1995; 95US-0483528.
XX
XX 07-JUN-1995; 95US-0483528.
XX
XX 07-SEP-1993; 93US-0116778.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Hasegawa M, Kolke M, Kuvana Y, Nakamura K;
XX Shitara K;
XX WPI, 1999-468416/39.
XX P-PSDB; AAY28359.
XX
XX Chimeric human antibody expression vectors
XX
XX Example 1; Column 87-89; 188pp; English.
XX
XX This antibody chain is derived from Hybridoma cells producing the Rat
XX Anti-GM2 Monoclonal Antibody KM-603.
XX The chimeric human antibodies are useful in the treatment of
XX cancer, especially that which is of neural ectodermal origin.
XX In contrast to prior art constructs based on mouse monoclonal
XX antibodies, the chimeric human antibodies do not cause anti-mouse
XX immunoglobulin production.
XX The chimeric human antibodies have a prolonged half-life and a reduced
XX frequency of adverse effects when compared to mouse monoclonal
XX antibodies.
XX
SQ Sequence 405 BP; 95 A; 110 C; 103 G; 97 T; 0 other;

alignment_scores:
Quality: 388.50 Length: 121
Ratio: 3.809 Gaps: 1
Percent Similarity: 84.298 Percent Identity: 62.810

alignment_block:
US-09-786-015-2 x AAx9477 ..

Align seg 1/1 to: AAx9477 from: 1 to: 405

```
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
67 CAAGTCAGCTGAAGAGGAGTCAGACCTGCTGCTGTCAGCCCTCACAGAC 116
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
117 CCGTCCCTCACCCTGCACCTGCTCTGCGTCTCATTAACACGCTATACTG 166
```

```

34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
167 TAAAGCTGGTGGCCAGCTCCAGGAAGGCTCGAGTGTGACAGCA 216
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
:::|||||
217 ATATCAAGTGTGGAGCACAATATTAATTCACCTCTCAAAATCAGACT 266
67 userValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||
267 GAGCATCAGACAGGAGCAGCTCCAGACCAAGTTTCTTAAAAATGAACA 316
84 erValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
|||||
317 GTCGCAAACTGGAAGACACAGCCATGACTCTCTGCCCCCTTCGAGGG 366
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
:::
367 GCC.....TGGGGCCAGGAGTCATGCT 389
117 uThrValSerSer 121
:::
390 CACAGCTCCTCA 402

```

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:AAQ13110

seq_documentation_block:

ID AAQ13110 standard; DNA; 407 BP.

XX AAQ13110;

DT 21-OCT-1991 (first entry)

XX HuVhlys.

XX Hypervariable region; light chain; heavy chain; CDR; RBS; antigen; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT CDS 10..369

FT /tag= a

FT /label= HuVhlys

FT misc_RNA 112..126

FT /tag= b

FT /label= CDR1

FT misc_RNA 169..216

FT /tag= c

FT /label= CDR2

FT misc_RNA 311..336

FT /tag= d

FT /label= CDR3

XX EP440146-A.

PN EP440147-A.

XX 07-AUG-1991.

PD 28-JAN-1991.

PF 91BP-0101094.

XX 09-FEB-1990.

PR 90DE-4003880.

PR 01-FEB-1990.

XX 90DE-4002897.

XX (BEHW) BEHRINGER AG.

XX Little M, Bretling FB, Seehaus T, Dubel S, Kiewinghaus I;

PI WPI; 1991-231878/32.

XX Synthetic human antibody library - produced by expression of DNA

PT confg. random sequences for hyper-variable regions

XX Disclosure; Page 10; 14pp; German.

```

XX Synthetic human antibody libraries can be produced by using
CC randomly synthesised oligonucleotides coding for each of the three
CC hypervariable regions in the variable parts of the heavy and light
CC chains (regions CDR1, CDR2 and CDR3). Two batches of oligonucleotides
CC are used for the synthesis of the variable domains. These are
CC ligated and inserted into expression vector pFMT.
CC pFMT (EP-440147) comprises a modified pRR233-2 plasmid (SalI-BamHI
CC deleted, HindIII replaced by BamHI) with an insert comprising a
CC first leader sequence (P1) (AAQ13098) from a bacterial peptidase
CC gene, a sequence (VH) (AAQ13110) coding for the variable domain of a
CC human antibody heavy chain (HuVhlys), a ribosome binding site (RBS),
CC a second leader sequence (P2) (AAQ13099), and a sequence (VL)
CC (AAQ13111) coding for the variable domain of a human antibody light
CC chain (HuVllys). TAG sequences are represented in AAQ13108-09.
CC The libraries may be used to isolate clones producing specific
CC antibodies or antigen-binding antibody fragments by screening with
CC specific antigens.
XX
SQ Sequence 407 BP; 98 A; 111 C; 104 G; 94 T; 0 other;

```

alignment_scores:

Quality: 388.50 Length: 121

Ratio: 3.847 Gaps: 1

Percent Similarity: 83.471 Percent Identity: 62.810

alignment_block:

US-09-786-015-2 x AAQ13110 ..

Align seg 1/1 to: AAQ13110 from: 1 to: 407

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1 GlnValGlnLeuGlnGlnUserGlyProSerLeuValLysProSerGlnTh 17
|||||
22 CAGGTCCAACTGACGAGAGCGGTCACGCTCTGTGAGACTGACCCAGAC 71
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrcysGly 34
|||||
72 CCGTAGCCCTGACGACCGGTGCTGCTCACCCTGACGCGCATGTG 121
34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
122 TAAAGCTGGTGGAGACACCACTGAGAGGTCTGAGTGTGATGAGATG 171
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
:::
172 ATTGGGGTGATGGAACACAGACTATTAATTCACCTCTCAAAATCAGAGT 221
67 userValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
:::
222 GACAATGCTGTGAGACACAGCAAGACGTTCCAGCTGAGACTGAGCA 271
84 erValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
|||||
272 GCGTGACAGCCGCCGACACCGGCTATTAATTTGTGCAAGAGAGAGATG 321
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
:::
322 .....TAPAGGCTTGACTACTGCGGGGTGACGGGCTCCCTCGT 356
117 uThrValSerSer 121
:::
357 CACAGTCTCCTCA 369

```

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AA134095

seq_documentation_block:

ID AA134095 standard; DNA; 357 BP.

XX AA134095;

AC 12-OCT-1996 (first entry)

XX

DT

XX

```

DE  NEMM humanised 2B6 antibody heavy chain variable region DNA.
XX
KW  Antibody engineering; humanised antibody; chimeric antibody; Fab;
KW  Interleukin-5; IL-5; eosinophil; asthma; allergic rhinitis;
KW  atopic dermatitis; therapy; diagnosis; heavy chain; VH;
KW  monoclonal antibody; Mab; ss.
XX
OS  Synthetic.
XX
PN  WO9621000-A2.
XX
PD  11-JUL-1996.
XX
PF  22-DEC-1995; 95MO-US17082.
XX
XX  06-JUN-1995; 95US-0470110.
PR  23-DEC-1994; 94US-0363131.
PR  06-JUN-1995; 95US-0467420.
XX
PA  (SMIK ) SMITHKLINE BEECHAM CORP.
PA  (SMIK ) SMITHKLINE BEECHAM PLC.
PI  Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;
PI  Holmes SD, McMillan LJ, Theisen TW;
XX  WPI; 1996-333976/33.
DR  P-PSDB; AAR98492.
XX
XX  New monoclonal antibody to human interleukin-5 - used to produce
PT  products for the treatment and diagnosis of conditions associated
PT  with excess eosinophil prodn., e.g asthma etc.
PS
PS  Example 4; Page 86-87; 120pp; English.
XX
XX  A synthetic DNA sequence (AAT34095) codes for the heavy chain variable
CC  region (AAR98492) of NEMM humanised antibody 2B6 comprising
CC  complementarity determining regions (see also AAR98460-62) derived from
CC  murine monoclonal antibody 2B6 VH (see also AAR98478) and framework
CC  regions from human immunoglobulin NPM, but with amino acid
CC  substitutions made at framework residues that might influence CDR
CC  presentation. A synthetic variable light chain sequence (AAT34096)
CC  was also constructed. Humanised 2B6 (see also AAT34093-94) is
CC  specific for human Interleukin-5 (IL-5) and can be used for the
CC  diagnosis and treatment of IL-5-mediated conditions, e.g. asthma,
CC  allergic rhinitis and atopic dermatitis.
XX
XX  Sequence 357 BP; 82 A; 103 C; 98 G; 74 T; 0 other;
SO

```

```

151 AATAGGGCTAGTGGAGGCGACACATTATATATTCGGCTCTCAGTCCAGACT 200
67 uSerValThrArgAspPthSerLysSerClnPheSerLeuSerLeuSers 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 GAGTATTACTGAGAAGACACACAGACACACAGCTGACCTGAGACTCAGCA 250
84 eValThrThrClnuSpThrAlaIleTyrTyrCysAluLysSerValasn 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 GCGTAGCAGCCGCCGACACCGCGGCTCTATTACTGTGCTCG.....GAT 294
101 GtAspSerValProTyrCtLLeuaspTyrTrpSerProGtlyLeuLeu 117
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
295 CCCCCCTTCTCTTACTACTAGCGCTTACTACTACTGCGACAGGTACCGCGT 344
117 uThrValSerSer 121
:|||||:|||||:
345 CACCGTCTCGAGC 357

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:AAQ31365
seq_documentation_block:
ID AAQ31365 standard; DNA; 438 bp.
XX
AC AAQ31365;
XX
DT 30-MAR-1993 (first entry)
XX
DE pUC-RVh-PM1f-4.
XX
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KM complementarily determining region; mouse; monoclonal; hybrldoma;
RV plasmid; polymerase chain reaction; amplify; ss.
OS
XX Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 12..425
FT FT /*tag= a
FT FT stg_peptide 12..68
FT FT /*tag= b 69..425
FT FT mat_peptide /*tag= c
FT FT
XX
XX WO9219759-A.
XX
XX 12-NOV-1992.
XX
XX 24-APR-1992; 92WO-JP00544.
XX
XX 25-APR-1991; 91JP-0095476.
XX
XX 19-FEB-1992; 92JP-0032084.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX
XX Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
XX
XX WPI: 1992-398882/48.
XX
XX DR P-PSDB: AAR29014.
XX
XX
XX Reconstituted human antibody to human interleukin-6 receptor -
XX
XX PT has low antigenicity and contains mouse V-region complementary
XX
XX PT determining regions
XX
XX
XX Disclosure; Page 142-3; 207pp; Japanese.
XX
XX
XX The sequences given in AAQ31360-61 and AAQ31365-66 are plasmids encoding
XX
XX CC portions of monoclonal antibodies which were derived from mouse
XX
XX CC hybridomas. The DNA encoding complementarity determining regions
XX
XX CC (CDR's) was isolated by polymerase chain reaction. The antibodies
XX
XX CC produced recognises human interleukin-6 receptor (IL-6R). The
XX
XX CC hybrldoma cells were transformed with plasmids containing fragments
XX
XX CC of the antibody gene which caused the production of the antibody from
XX
XX CC the hybrldoma cells.

```

XX Sequence 438 BP; 105 A; 123 C; 113 G; 97 T; 0 other;
SQ

alignment_scores:

Quality:	384.00	Length:	122
Ratio:	3.657	Gaps:	2
Percent Similarity:	86.066	Percent Identity:	61.475

alignment_block:

us-09-786-015-2 x AAQ31365 ..

Align seg 1/1 to: AAQ31365 from: 1 to: 438

```
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
69 CAGGTCCAATGACAGAGAGCGGTCCAGGTCTGTGTGAGACCTAGCCAGAC 118
|||||
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLys...TyrG 33
|||||
119 CCTGAGAGCTGACCTGCACCGTGTCTGCTACTCATATTACCGAGATCATG 168
|||||
33 lYValSerTPValArgGlnAlaProGlyLysAlaLeuGlnUTrPLeuGly 49
::: |||||||
169 CCTGAGAGCTGGGTTCCGCCAGCCACCTGGACGAGGCTTGTGAGTGATTGA 218
|||||
50 GlyValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerAr 66
::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
219 TACATTAGTATATAGTGAATACACACTATATCATCTCTCAATTCAG 268
|||||
66 gLeuSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeus 83
::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
269 AGTGACATATGCTGAGACACACAGCAAGAACCATTCAGCCTGAGACTCA 318
|||||
83 eSerValThrThrGlnAspThrAlaIleTyrThrCysAlaLysSerVal 99
|||||
319 GCAGCGTGACAGCCGCCGACACCGGCTTATTTATTTGTGCAGATCCCTA 368
|||||
100 AsnGlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLe 116
::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
369 GCTCGGACTACG.....GCTATGACTACTGGGGTCAAGGCAGCCT 409
|||||
116 uLeuThrValSerSer 121
|||||
410 GGTACACAGTCTCTCA 425
```